

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2005, 09:19:07 ; Search time 70 Seconds
(without alignments)
243.107 Million cell updates/sec

Title: US-10-031-005-3

Perfect score: 192
Sequence: 1 ANAFLLXLRPGSLRXKCKX.....XXARXIFKDAKXRTKLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	89.6	44	2 AAY18305	Aay18305 Human fac
2	172	89.6	44	4 AAB36395	Aab36395 Human fac
3	172	89.6	44	7 ADD50096	Add50096 Human vit
4	172	89.6	44	8 ADQ26902	Adq26902 Human fac
5	172	89.6	401	4 AAB84870	Aab84870 Mutant bl
6	172	89.6	401	4 AAB84871	Aab84871 Mutant bl
7	172	89.6	406	2 AAR35764	Aar35764 Factor VI
8	172	89.6	406	2 AAW14510	Aaw14510 Modified
9	172	89.6	406	2 AAW14509	Aaw14509 Modified
10	172	89.6	406	4 AAU77745	Aau77745 Human fac
11	172	89.6	406	4 AAB84867	Aab84867 Mutant bl
12	172	89.6	406	4 AAB84868	Aab84868 Mutant bl
13	172	89.6	406	4 AAB84869	Aab84869 Mutant bl
14	172	89.6	406	4 AAB84866	Aab84866 Wild-type
15	172	89.6	406	4 AAB84865	Aab84865 Human FVI
16	172	89.6	406	4 AAM52172	Aam52172 Mammalian
17	172	89.6	406	4 AAM52186	Aam52186 Human FVI
18	172	89.6	406	4 AAM52171	Aam52171 Human FVI
19	172	89.6	406	4 AAM52187	Aam52187 Human FVI
20	172	89.6	406	4 AAM52181	Aam52181 Human FVI
21	172	89.6	406	4 AAM52185	Aam52185 Human FVI
22	172	89.6	406	4 AAM52184	Aam52184 Human FVI
23	172	89.6	406	4 AAM52182	Aam52182 Human FVI
24	172	89.6	406	5 AAU77196	Aau77196 Human coa
25	172	89.6	406	5 AAU77191	Aau77191 Human coa

26	172	89.6	406	5 AAU77200	Aau77200 Human coa
27	172	89.6	406	5 AAU77192	Aau77192 Human coa
28	172	89.6	406	5 AAU77190	Aau77190 Human coa
29	172	89.6	406	5 AAU77198	Aau77198 Human coa
30	172	89.6	406	5 AAU77193	Aau77193 Human coa
31	172	89.6	406	5 AAU77199	Aau77199 Human coa
32	172	89.6	406	5 AAU79201	Aau79201 Human coa
33	172	89.6	406	5 AAU77188	Aau77188 Human coa
34	172	89.6	406	5 AAU77194	Aau77194 Human coa
35	172	89.6	406	5 AAU77195	Aau77195 Human coa
36	172	89.6	406	5 AAU77189	Aau77189 Human coa
37	172	89.6	406	5 AAU77197	Aau77197 Human coa
38	172	89.6	406	5 ABG31688	Abg31688 Human coa
39	172	89.6	406	5 ABB09178	Abb09178 Human fac
40	172	89.6	406	5 ABB80051	Abb80051 Human coa
41	172	89.6	406	5 ABB80069	Abb80069 Human coa
42	172	89.6	406	5 ABB80072	Abb80072 Human coa
43	172	89.6	406	5 ABB80071	Abb80071 Human coa
44	172	89.6	406	5 ABB80068	Abb80068 Human coa
45	172	89.6	406	5 ABB80070	Abb80070 Human coa

ALIGNMENTS

RESULT 1
AAY18305
ID AAY18305 standard; peptide; 44 AA.
XX
AC AAY18305;
XX
DT 17-AUG-1999 (first entry)
XX
DE Human factor VII GLA domain.
XX
KW GLA domain; vitamin K-dependent protein; clotting disorder; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..44
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
FT
XX
PN WO9920767-Al.
XX
PD 29-APR-1999.
XX
PF 20-OCT-1998; 98WO-US022152.
XX
PR 23-OCT-1997; 97US-00955636.
XX
PA (MINU) UNIV MINNESOTA.
XX
PI Nelsestuen GL;
XX
DR WPI; 1999-288309/24.
XX
PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders.
XX
PS Disclosure; Page 15; 86pp; English.
XX
CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein
XX
SQ Sequence 44 AA;

Query Match 89.6%; Score 172; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ANAFLLXLRPGSLRXKXCKXQCSPFXARXIFKDAARTKLFWISY 44
|||||
DB 1 ANAFLLXLRPGSLRXKXCKXQCSPFXARXIFKDAARTKLFWISY 44
|||||

RESULT 2
AAB36395
ID AAB36395 standard; peptide; 44 AA.
XX AC AAB36395;
XX XX
DT 27-FEB-2001 (first entry)
XX XX
DE Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
XX XX
KW Vitamin K-dependent protein; factor VII; protein C; GLA domain;
KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
KW factor X; prothrombin; enhanced membrane binding affinity;
KW clot formation; thrombolytic; haemostatic; bleeding disorder; thrombosis;
KW clotting disorder; haemophilia A; haemophilia B; liver disease.
XX XX
OS Homo sapiens.
XX XX
FN WO200066753-A2.
XX XX
PD 09-NOV-2000.
XX XX
PF 28-APR-2000; 2000WO-US011416.
XX XX
PR 29-APR-1999; 99US-00302239.
XX XX
PA (MINU) UNIV MINNESOTA.
XX XX
PI Nelseestuen GL;
XX XX
DR WPI; 2001-007226/01.
XX XX

Novel vitamin K-dependent polypeptide useful for treating clotting disorders such as thrombosis and hemophilia, comprises modified gamma-carboxy glutamic acid domain that enhances membrane binding affinity.

PS Disclosure; Page 12; 81pp; English.

CC The present invention describes a vitamin K-dependent polypeptide (I) comprising a modified gamma-carboxy glutamic acid (GLA) domain having at least one amino acid substitution, that enhances membrane binding affinity and the activity of the polypeptide relative to a corresponding native vitamin K-dependent polypeptide and inhibits clot formation. (I) can have thrombolytic and haemostatic activities, and can be used as an inhibitor of clot formation. (II) is useful for decreasing clot formation in a mammal, a factor VII or factor IX containing a modified GLA domain is useful for increasing clot formation and for treating a bleeding disorder, including thrombosis and clotting disorders such as haemophilia A, haemophilia B and liver disease. The present sequence represents a wild type human factor VII GLA domain sequence, given in the exemplification of the present invention

XX Sequence 44 AA;

Query Match 89.6%; Score 172; DB 4; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ANAFLLXLRPGSLRXKXCKXQCSPFXARXIFKDAARTKLFWISY 44
|||||
DB 1 ANAFLLXLRPGSLRXKXCKXQCSPFXARXIFKDAARTKLFWISY 44
|||||

RESULT 3
ADD50096
ID ADD50096 standard; protein; 44 AA.
XX AC ADD50096;
XX XX
DT 15-JAN-2004 (first entry)
XX XX
DE Human vitamin K-dependent protein #2.

XX KW Human; vitamin K-dependent protein; gamma-carboxyglutamic acid domain;
KW GLA domain; membrane binding affinity; clot formation; haemophilia;
KW clotting disorder; site directed mutagenesis; haemostatic; anticoagulant;
KW thrombolytic.

XX OS Homo sapiens.

XX FN US2003100506-A1.

XX XX 29-MAY-2003.

XX PF 18-NOV-2002; 2002US-00299330.

XX XX 23-OCT-1997; 97US-00955636.

PR 29-APR-1999; 99US-00302239.

PR 03-FEB-2000; 2000US-00497591.

XX XX (NELS/) NELSESTUEN G L.

XX XX Nelseestuen GL;

XX XX WPI; 2003-606646/57.

XX PT New vitamin K-dependent polypeptide for modulating clot formation in mammals comprises a modified gamma-carboxyglutamic acid domain that enhances membrane binding affinity and activity of the polypeptide.

XX PS Example 5; SEQ ID NO 3; 51pp; English.

XX CC The invention relates to a vitamin K-dependent polypeptide comprising a modified gamma-carboxyglutamic acid (GLA) domain that enhances membrane binding affinity and activity of the polypeptide relative to a corresponding native vitamin K-dependent polypeptide, where the modified GLA domain comprises a glutamic acid residue at position 34. The polypeptide is useful in modulating clot formation in mammals or in treating certain types of haemophilia or clotting disorders. The membrane binding affinity of polypeptides is increased by site directed mutagenesis in the GLA domain. This sequence represents a vitamin K-dependent protein of the invention.

XX SQ Sequence 44 AA;

Query Match 89.6%; Score 172; DB 7; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ANAFLLXLRPGSLRXKXCKXQCSPFXARXIFKDAARTKLFWISY 44
|||||

DB 1 ANAFLLXLRPGSLRXKXCKXQCSPFXARXIFKDAARTKLFWISY 44
|||||

RESULT 4

ADQ26902
ID ADQ26902 standard; protein; 44 AA.

XX AC ADQ26902;

XX DT 26-AUG-2004 (first entry)

XX DE Human factor VII gamma-carboxyglutamic acid (GLA) domain.

XX XX Human; clot formation; protein C; activated protein C; APC;

KW gamma-carboxyglutamic acid domain; GLA domain; vitamin K-dependent;

DR N-PSDB; AAH19464.

XX Mutant of blood coagulant factor VII, used for substitution therapy in
PT the treatment of hemophilia.
XX Claim 16; Page 23-24; 29pp; Japanese.
PS The present invention relates to mutants of blood coagulant factor VII
CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
CC sequence is one such mutant FVII: VII-39. The mutants can be used as an
CC agent for the substitution therapy of haemophilia inhibitor patients
XX
SQ Sequence 401 AA;
Query Match 89.6%; Score 172; DB 4; Length 401;
Best Local Similarity 77.3%; Pred. No. 1.2e-20;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 1 ANAFLLXLRPGSLRXKXKXQCSFXXARXIFKDAERTKLFWISY 44
Db 1 ANAFLELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 44
RESULT 7
AAR35764
ID AAR35764 standard; protein; 406 AA.
XX AC AAR35764;
XX
DT 25-MAR-2003 (revised)
DT 24-SEP-1993 (first entry)
XX
DE Factor VII (VII).
XX
KW PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;
KW Factor VII; CT; chymotrypsinogen; SP; serine protease; binding; exosite;
KW catalytic activity.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..152
FT /note= "Factor VII light chain"
FT Region 153..406
FT /note= "Factor VII heavy chain"
FT Peptide 245..266
FT /note= "Claim 9, page 138-139 describes an antibody that
FT reacts with Factor VII; fragments 289-304, 290-304, 290-
FT 310, 374-388 and 400-414 but not with fragment 245-266"
FT Peptide 289..304
FT /note= "pref. PC polypeptide; claim 4, page 137"
FT Peptide 290..310
FT /note= "exosite 2"
FT Peptide 290..310
FT /note= "pref. PC polypeptide; claim 2, page 136"
FT Peptide 290..304
FT /note= "pref. PC polypeptide; claim 4, page 137"
FT Peptide 374..388
FT /note= "exosite 1"
FT Peptide 374..388
FT /note= "pref. PC polypeptide; claim 2, page 136"
XX
XX WO9309804-A1.
XX
PD 27-MAY-1993.
XX
PF 18-NOV-1992; 92WO-US010242.
XX
PR 18-NOV-1991; 91US-00793989.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Griffin JH, Meesters RM;
XX

DR WPI; 1993-182244/22.
XX Serine protease derived-polypeptide(s) and anti-peptide antibodies - for
PT inhibiting coagulation and assaying for the presence of serine protease
PT in fluid samples.
XX
PS Disclosure; Page 133-135; 149pp; English.
XX
CC The PC polypeptides indicated in the Features Table inhibit coagulation
CC (they prevent binding of serine protease to natural substrates), esp.
CC when admin. to give an intravascular blood concn. of 0.1-100 (pref. 0.5-
CC 10) microm. NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are
CC described in the specification but have not yet been added to the
CC SEQUENCE LISTING. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 406 AA;
Query Match 89.6%; Score 172; DB 2; Length 406;
Best Local Similarity 77.3%; Pred. No. 1.2e-20;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 1 ANAFLLXLRPGSLRXKXKXQCSFXXARXIFKDAERTKLFWISY 44
Db 1 ANAFLELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 44
RESULT 8
AAW14510
ID AAW14510 standard; protein; 406 AA.
XX AC AAW14510;
XX
DT 25-MAR-2003 (revised)
DT 14-MAY-1997 (first entry)
XX
DE Modified blood coagulation Factor VII (R315S).
XX
KW Blood coagulation; factor 7; mutein; mutation; modification;
KW thrombocytopenia; von Willebrand's disease; plasma substitute.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 6
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 7
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 14
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 16
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Disulfide-bond 17..22
FT Modified-site 19
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 20
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 25
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 26
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 29
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Cleavage-site 32..33

FT	Modified-site	35	/note= "proteolytic site"
FT			/label= OTHER
FT			/note= "gamma-carboxyglutamic acid"
FT	Cleavage-site	38. .39	/note= "proteolytic site"
FT			/note= "proteolytic site"
FT	Cleavage-site	42. .43	/note= "proteolytic site"
FT			/note= "proteolytic site"
FT	Cleavage-site	44. .45	/note= "proteolytic site"
FT			/note= "proteolytic site"
FT	Disulfide-bond	50. .61	
FT	Disulfide-bond	55. .70	
FT	Modified-site	63	/label= OTHER
FT			/note= "beta-hydroxy-aspartic acid"
FT	Disulfide-bond	72. .81	
FT	Disulfide-bond	91. .102	
FT	Disulfide-bond	98. .112	
FT	Disulfide-bond	114. .127	
FT	Disulfide-bond	135. .162	
FT	Cleavage-site	143. .144	/note= "proteolytic site"
FT			/note= "proteolytic site"
FT	Modified-site	145	
FT			/note= "glycosylation site"
FT	Disulfide-bond	159. .164	
FT	Disulfide-bond	178. .194	
FT	Active-site	193	
FT	Active-site	242	
FT	Cleavage-site	290. .291	
FT			/note= "proteolytic site"
FT	Disulfide-bond	310. .329	
FT	Cleavage-site	315. .316	/note= "proteolytic site in unmodified factor VII"
FT	Misc-difference	315	
FT			/note= "native Arg315 has been substituted by Ser to provide a proteolytically more stable peptide bond"
FT			
FT	Modified-site	322	/note= "glycosylation site"
FT	Disulfide-bond	340. .368	
FT	Cleavage-site	341. .342	/note= "proteolytic site"
FT			/note= "proteolytic site"
FT	Active-site	344	
FT	Cleavage-site	392. .393	
FT			/note= "proteolytic site"
FT	Cleavage-site	396. .397	/note= "proteolytic site"
FT			/note= "proteolytic site"
FT	Cleavage-site	402. .403	/note= "proteolytic site"
FT			/note= "proteolytic site"
XX			
PN	US5580560-A.		
XX			
PD	03-DEC-1996.		
XX			
PF	22-AUG-1994;	94US-00293778.	
XX			
PR	13-NOV-1989;	89US-00434149.	
PR	12-JUN-1992;	92US-00898248.	
PR	09-AUG-1993;	93US-00104509.	
XX			
XX	(NOVO) NOVO-NORDISK AS.		
XX			
PI	Wiberg FC, Woodbury R, Nicolaisen EM, Bjorn SE;		
XX			
DR	WPI; 1997-033523/03.		
XX			
XX	Mutated human factor VII or VIIa proteins - with amino acid substitutions to improve proteolytic stability.		
FT			
XX			
PS	Example 4; Page; 28pp; English.		
XX			
CC	Modified human factor VII or VIIa proteins are stabilised against proteolytic cleavage by substitution of one of the residues Lys32, Lys38, Ile42, Tyr44, Phe378, Arg290, Arg304, Tyr332 and Lys341 by an		

CC	amino acid that provides a proteolytically more stable peptide bond.
CC	provided that Lys32 is replaced by Gln, Glu, His, Gly, Thr, Ala or Ser.
CC	The modified proteins are useful for treating bleeding disorders such as
CC	thrombocytopenia and von Willebrand's disease. They are also suitable for
CC	addition to plasma substitutes. The present sequence is a specific
CC	example of a modified factor VII protein. (Updated on 25-MAR-2003 to
CC	correct PF field.)
XX	
SQ	Sequence 406 AA;
	Query Match 89.6%; Score 172; DB 2; Length 406;
	Best Local Similarity 77.3%; Pred. No. 1.2e-20;
	Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy	1 ANAFLLXLRPGSLRXKXCKXCSCFXXARXIFKDAARTKLFWISY 44
Db	1 ANAFLEELRPGSLRECKEKCSCFEAREIFKDAERTKLFWISY 44
RESULT 9	
AAW14509	
ID	AAW14509 standard; protein; 406 AA.
XX	
AC	AAW14509;
XX	
XX	25-MAR-2003 (revised)
DT	14-MAY-1997 (first entry)
XX	
DE	Modified blood coagulation Factor VII (R290S).
XX	
KW	Blood coagulation; factor 7; mutant; mutation; modification;
KW	thrombocytopenia; von Willebrand's disease; plasma substitute.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PH	Key
FT	Modified-site 6
FT	/label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Modified-site 7
FT	/label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Modified-site 14
FT	/label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Modified-site 16
FT	/label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Disulfide-bond 17. .22
FT	Modified-site 19
FT	/label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Modified-site 20
FT	/label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
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FT	Modified-site 25
FT	/label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Modified-site 26
FT	/label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Modified-site 29
FT	/label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Cleavage-site 32. .33
FT	/label= OTHER
FT	/note= "proteolytic site"
FT	
FT	Modified-site 35
FT	/label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Cleavage-site 38. .39
FT	/label= OTHER
FT	/note= "proteolytic site"
FT	
FT	Cleavage-site 42. .43

FT Cleavage-site /note= "proteolytic site"
FT 44. .45
FT /note= "proteolytic site"
FT 50. .61
FT Disulfide-bond
FT Disulfide-bond 55. .70
FT Modified-site 63
FT /label= OTHER
FT /note= "beta-hydroxy-aspartic acid"
FT 72. .81
FT Disulfide-bond 91. .102
FT Disulfide-bond 98. .112
FT Disulfide-bond 114. .127
FT Disulfide-bond 135. .162
FT Cleavage-site 143. .144
FT /note= "proteolytic site"
FT 145
FT Modified-site /note= "glycosylation site"
FT 159. .164
FT Disulfide-bond 178. .194
FT Active-site 193
FT Active-site 242
FT Cleavage-site 290. .291
FT /note= "proteolytic site in unmodified factor VII"
FT Misc-difference 290
FT /note= "native Arg290 has been substituted by Ser to
FT provide a proteolytically more stable peptide bond"
FT 310. .329
FT Cleavage-site 315. .316
FT /note= "proteolytic site"
FT 322
FT Modified-site /note= "glycosylation site"
FT 340. .368
FT Disulfide-bond 341. .342
FT Cleavage-site /note= "proteolytic site"
FT 344
FT Active-site 392. .393
FT Cleavage-site /note= "proteolytic site"
FT 396. .397
FT Cleavage-site /note= "proteolytic site"
FT 402. .403
FT Cleavage-site /note= "proteolytic site"
FT
FT
PN US5580560-A.
XX
XX 03-DEC-1996.
XX
XX 22-AUG-1994; 94US-00293778.
XX
XX 13-NOV-1989; 89US-00434149.
XX 12-JUN-1992; 92US-00898248.
XX 09-AUG-1993; 93US-00104509.
XX
XX (NOVO) NOVO-NORDISK AS.
XX
XX Wiberg FC, Woodbury R, Nicolaisen EM, Bjorn SE;
XX WPI; 1997-033523/03.
XX
XX Mutated human factor VII or VIIa proteins - with amino acid substitutions
XX to improve proteolytic stability.
XX
XX Example 3; Page; 28pp; English.
XX
XX Modified human factor VII or VIIa proteins are stabilised against
XX proteolytic cleavage by substitution of one of the residues Lys32, Lys38,
XX Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and Lys341 by an
XX amino acid that provides a proteolytically more stable peptide bond,
XX provided that Lys32 is replaced by Gln, Glu, His, Gly, Thr, Ala or Ser.
XX The modified proteins are useful for treating bleeding disorders such as
XX thrombocytopenia and von Willebrand's disease. They are also suitable for
XX addition to plasma substitutes. The present sequence is a specific
XX example of a modified factor VII protein. (Updated on 25-MAR-2003 to
XX correct PF field.)

XX SQ Sequence 406 AA;
XX
XX Query Match 89.6%; Score 172; DB 2; Length 406;
XX Best Local Similarity 77.3%; Pred. No. 1.2e-20;
XX Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
XX
XX Qy 1 ANAFLLXLRPGSLRXCKXQCSFXXARXIFKDXARTKLFWISY 44
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX Db 1 ANAFLEELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 44
XX
XX RESULT 10
XX AAU77745
XX ID AAU77745 standard; protein; 406 AA.
XX
XX AC AAU77745;
XX
XX 05-JUN-2002 (first entry)
XX
XX Human factor VIIa active site mutant.
XX
XX Factor VIIa; human; shock heat treatment; protein stability;
XX protein manufacture; protein conformation; mutant; mutein.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Active-site 193
XX /note= "Member of the factor VIIa catalytic triad"
XX Active-site 242
XX /note= "Member of the factor VIIa catalytic triad"
XX Misc-difference 344
XX /label= Gly, Met, Thr
XX /note= "Preferably Ala. Wild type Ser"
XX Active-site 344
XX /note= "Member of the factor VIIa catalytic triad"
XX
XX WQ20017141-A1.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-DK000234.
XX
XX 06-APR-2000; 2000DK-00000573.
XX 17-APR-2000; 2000US-0197850P.
XX
XX (NOVO) NOVO NORDISK AS.
XX
XX Matthiesen F;
XX
XX WPI; 2001-657162/75.
XX
XX Stabilization of a polypeptide e.g. in a pharmaceutical composition
XX involves a shock heat treatment.
XX
XX Disclosure; Page; 22pp; English.
XX
XX The invention describes a method of stabilising a polypeptide involving
XX shock heat treatment of the polypeptide. The method is useful in a
XX pharmaceutical composition, in the industrial or large scale method of
XX manufacturing a polypeptide, also as a unit operation during preparation,
XX purification, recovery and/or formulation of polypeptides. The shock heat
XX treatment improves the protein stability without substantial loss of
XX biological activity. The method can be applied to change polypeptide
XX conformation in a very fast and non-invasive manner. The polypeptide
XX formed is stable. The method is also useful for decreasing the
XX association of the polypeptide. This sequence represents a modified human
XX factor VIIa protein mutated at the catalytic site, described in the
XX invention. Note: This sequence does not appear in the specification but
XX has been obtained using information given in the invention
XX

```

SQ      Sequence 406 AA;
Query Match      89.6%; Score 172; DB 4; Length 406;
Best Local Similarity 77.3%; Pred. No. 1.2e-20;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy      1 ANAFLLXLRPGSLRXRCXXQCSPFXKXARXIFKDAKRTKLFWISY 44
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 ANAFLELRPGSLRECKEQQCFEAREIFKDAERTKLFWISY 44

RESULT 11
AAB84867
ID      AAB84867 standard; protein; 406 AA.
XX
AC      AAB84867;
XX
DT      31-JUL-2001 (first entry)
XX
DE      Mutant blood coagulant factor VII (FVII-5).
XX
KW      Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KW      mutant; mutain.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
FH      Key Location/Qualifiers
FT      Misc-difference 159
      /note= "Wild-type Cys substituted by Ala"
FT      Misc-difference 164
      /note= "Wild-type Cys substituted by Ala"
FT      Misc-difference 164
      /note= "Wild-type Cys substituted by Ala"
XX
PN      JP2001061479-A.
XX
PD      13-MAR-2001.
XX
PF      24-AUG-1999; 99JP-00237610.
XX
PR      24-AUG-1999; 99JP-00237610.
XX
PA      (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
DR      WPI; 2001-310677/33.
DR      N-PSDB; AAH19461.
XX
FT      Mutant of blood coagulant factor VII, used for substitution therapy in
      the treatment of hemophilia.
XX
PS      Claim 5; Page 14-15; 29pp; Japanese.
XX
CC      The present invention relates to mutants of blood coagulant factor VII
      (FVII) or activated blood coagulant factor VII (FVIIa). The present
      sequence is one such mutant FVII: VII-5. In the wild-type protein
      (AAB84866), there is a disulphide bond (159Cys-164Cys). In the present
      protein, the disulphide bond is disrupted. The mutants can be used as an
      agent for the substitution therapy of haemophilia inhibitor patients
XX
SQ      Sequence 406 AA;

Query Match      89.6%; Score 172; DB 4; Length 406;
Best Local Similarity 77.3%; Pred. No. 1.2e-20;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy      1 ANAFLLXLRPGSLRXRCXXQCSPFXKXARXIFKDAKRTKLFWISY 44
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 ANAFLELRPGSLRECKEQQCFEAREIFKDAERTKLFWISY 44

RESULT 12
AAB84868
ID      AAB84868 standard; protein; 406 AA.
XX
AC      AAB84868;
XX
DT      31-JUL-2001 (first entry)
XX
DE      Mutant blood coagulant factor VII (FVII-30).
XX
KW      Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KW      mutant; mutain.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
FH      Key Location/Qualifiers
FT      Misc-difference 235..239
      /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by Asp-

```

FT XX Arg-Lys-Thr-Leu"
 PN JP2001061479-A.
 XX
 PD 13-MAR-2001.
 XX
 PF 24-AUG-1999; 99JP-00237610.
 XX
 PR 24-AUG-1999; 99JP-00237610.
 XX
 PA (KAGA) ZH KAGAKU & KESSEI RYOHU KENKYUSHO.
 XX
 DR WPI; 2001-310677/33.
 DR N-PSDB; AAH19462.
 XX
 PT Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia.
 XX
 PS Claim 9; Page 17-18; 29pp; Japanese.
 CC The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-30. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients
 XX
 SQ Sequence 406 AA;
 Query Match 89.6%; Score 172; DB 4; Length 406;
 Best Local Similarity 77.3%; Pred. No. 1.2e-20;
 Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1 ANAFLLXLRPGSLRXKXQCSPFXARXIFKDAERTKLFWISY 44
 DB 1 ANAFLEELRPGSLRECKEBCQCFEAREIFKDAERTKLFWISY 44
 FT
 RESULT 14
 ID AAB84866
 AC AAB84866; standard; protein; 406 AA.
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Wild-type human blood coagulant factor VII (FVII).
 XX
 KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Disulfide-bond 159..164
 FT JP2001061479-A.
 XX
 PD 13-MAR-2001.
 XX
 PF 24-AUG-1999; 99JP-00237610.
 XX
 PR 24-AUG-1999; 99JP-00237610.
 XX
 PA (KAGA) ZH KAGAKU & KESSEI RYOHU KENKYUSHO.
 XX
 DR WPI; 2001-310677/33.
 DR N-PSDB; AAH19459.
 XX
 PT Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia.
 XX
 PS Disclosure; Page 8-9; 29pp; Japanese.
 CC The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present

CC sequence represents the protein sequence for wild-type human FVII. The
 CC mutants can be used as an agent for the substitution therapy of
 CC haemophilia inhibitor patients
 XX
 SQ Sequence 406 AA;
 Query Match 89.6%; Score 172; DB 4; Length 406;
 Best Local Similarity 77.3%; Pred. No. 1.2e-20;
 Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1 ANAFLLXLRPGSLRXKXQCSPFXARXIFKDAERTKLFWISY 44
 DB 1 ANAFLEELRPGSLRECKEBCQCFEAREIFKDAERTKLFWISY 44
 FT
 RESULT 15
 ID AAM52183
 AC AAM52183; standard; protein; 406 AA.
 XX
 DT 07-FEB-2002 (first entry)
 XX
 DE Human FVII mutant V253N.
 XX
 KW Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
 KW cardiant; hepatotropic; cerebroprotective; haemophilia; liver disease;
 KW myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
 KW mutein.
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 6
 FT /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 7
 FT /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 14
 FT /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 16
 FT /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 19
 FT /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 20
 FT /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 25
 FT /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 26
 FT /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 29
 FT /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 35
 FT /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT Modified-site 52
 FT /note= "O-glycosylated"
 FT Modified-site 60
 FT /note= "O-glycosylated"
 FT Modified-site 145
 FT /note= "N-glycosylated"
 FT Cleavage-site 152..153
 FT /notes= "proteolytic cleavage site converting FVII zymogen
 FT to an activated form, comprising two chains linked by a

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2005, 09:19:07 ; Search time 15 Seconds
(without alignments)
282.236 Million cell updates/sec

Title: US-10-031-005-3

Perfect score: 192

Sequence: 1 ANAFXXLRPGSLRXCKXX.....XXARXIFKDXRKLFWISY 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	89.6	466	1 KFHU7	coagulation factor
2	138	71.9	443	2 I46932	coagulation factor
3	123	64.1	407	1 KFB07	coagulation factor
4	109	56.8	461	1 JX0210	protein C (activat
5	104	54.2	456	1 KXBO	coagulation factor
6	102	53.1	488	1 EXHU	coagulation factor
7	101	52.6	492	1 EXBO	protein C (activat
8	100	52.1	461	1 S18994	coagulation factor
9	96	50.0	482	1 EXRT	coagulation factor
10	91	47.4	475	1 EXCH	coagulation factor
11	86	44.8	416	1 KFB0	protein C (activat
12	84	43.8	461	1 KXHU	coagulation factor
13	83	43.2	461	1 KFHU	thrombin (EC 3.4.2
14	83	43.2	622	1 TBHU	thrombin (EC 3.4.2
15	79	41.1	617	2 S10511	thrombin (EC 3.4.2
16	79	41.1	618	2 A35827	coagulation factor
17	78	40.6	452	1 A30351	coagulation factor
18	78	40.6	459	2 JQ0419	probable MAP kinase
19	71.5	37.2	576	2 G96763	probable MAP kinase
20	69	35.9	642	2 S53433	plasma protein S p
21	66	34.4	675	1 KXBOS	plasma protein S p
22	65.5	34.1	594	2 D84859	probable MAP kinase
23	65.5	34.1	603	2 C96575	probable MAP kinase
24	64	33.3	642	2 S53434	plasma protein S p
25	64	33.3	646	2 S38819	plasma protein S -
26	64	33.3	676	1 KXHUS	plasma protein Z p
27	63	32.8	396	1 KXBOZ	thrombin (EC 3.4.2
28	63	32.8	625	1 TBBO	thrombin (EC 3.4.2
29	63	32.8	675	1 KXRTS	plasma protein S p

RESULT 1

KFHU7

Coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human

C/Species: Homo sapiens (man)

C/Date: 19-May-1989 #sequence_revision 19-May-1994 #text_change 09-Jul-2004

C/Accession: A28322; A23819; A31186; B31186; S63524

R/O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; Murri

Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987

A/Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depende

A/Reference number: A28322; MUID:87260948; PMID:3037537

A/Accession: A28322

A/Molecule type: DNA

A/Residues: 1-466 <OHA>

A/Cross-references: UNIPROT:P08709; GB:J02933; NID:G180333; PIDN:AAA51983.1; PID:G180334

R/Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C.

Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986

A/Title: Characterization of a cDNA coding for human factor VII.

A/Reference number: A23819; MUID:86205965; PMID:3486420

A/Accession: A23819

A/Molecule type: mRNA

A/Residues: 1-466 <HAG>

A/Cross-references: GB:M13232; NID:G182799; PIDN:AAA8040.1; PID:G182801

R/Thim, L.; Bjoern, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.F

Biochemistry 27, 7785-7793, 1988

A/Title: Amino acid sequence and posttranslational modifications of human factor VII-a fi

A/Reference number: A90539; MUID:89088153; PMID:3264725

A/Accession: A31186

A/Molecule type: protein

A/Residues: 61-212 <THI>

A/Accession: B31186

A/Molecule type: protein

A/Residues: 213-466 <TH2>

R/Bjoern, S.; Foster, D.C.; Thim, L.; Wiberg, F.C.; Christensen, M.; Komiyama, Y.; Peders

J. Biol. Chem. 266, 11051-11057, 1991

A/Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations at

A/Reference number: A40529; MUID:91250411; PMID:1904059

A/Contents: annotation; carbohydrate binding sites

R/Persson, E.; Petersen, L.C.

Eur. J. Biochem. 234, 233-300, 1995

A/Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carboxy

A/Reference number: S63524; MUID:96096752; PMID:8529655

A/Accession: S63524

A/Molecule type: protein

C/Genetics:

A/Gene: GDB:F7

A/Cross-references: GDB:119897; OMIM:227500

A/Map position: 13q34-13q34

A/Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1

C/Function:

A/Description: catalyzes the proteolytic activation of coagulation factor X in the preser

coagulation factor IX in the presence of calcium and tissue factor

F;30-39/Domain: propeptide #status predicted <PRO>
F;40-194/Product: protein C light chain #status experimental <LCH>
F;98-128/Dmain: EGF homology <EG1>
F;137-172/Domain: EGF homology <EG2>
F;197-456/Product: protein C heavy chain #status experimental <HCH>
F;197-210/Dmain: activation peptide #status experimental <APT>
F;211-440/Dmain: trypsin homology <TRY>
F;45,46,53,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F;110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimen
F;119-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Bisulfide bonds: #stat
F;136,289,350/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;252,298,397/Active site: His, Asp, Ser #status predicted
F;366/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 54.2%; Score 104; DB 1; Length 456;
Best Local Similarity 45.5%; Pred. No. 1.3e-09;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLRXKXXCSPFXARXIFKDAXRTKLFWISY 44
|||:|||::| | | | | |||:
Db 40 ANSFLLELPNGVRECSSEVCFFEARIEIQNTDTWAFWSFY 83
|||:|||:

RESULT 6
EXHU
coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human
N;Alternate names: Stuart factor
C;Species: Homo sapiens (man)
C;Date: 15-Nov-1984 #sequence revision 02-May-1994 #text change 09-Jul-2004
C;Accession: A24478; JQ0917; A2485; A25853; A22208; A21284; A20362; S39415; I54051; A00
R;Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.
Biochemistry 25, 5098-5102, 1986
A;Title: Gene for Human Factor X: a blood coagulation factor whose gene organization is
A;Reference number: A24478; UID:87026600; PMID:3768336
A;Accession: A24478
A;Molecule type: DNA
A;Residues: 1-488 <LEV>
A;Cross-references: UNIPROT:P00742; GB:L29433; GB:M14327; NID:9459809; PIDN:AAA52764.1; I
R;Messier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.
Gene 99, 291-294, 1991
A;Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coag
A;Reference number: JQ0917; UID:91216473; PMID:1902434
A;Accession: JQ0917
A;Molecule type: mRNA
A;Residues: 1-488 <MES>
A;Cross-references: GB:M75285; NID:g182389; PIDN:AAA52421.1; PID:g182390
R;Wiao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.
J. Biol. Chem. 267, 7395-7401, 1992
A;Title: Liver-specific expression of the gene coding for human factor X, a blood coagul
A;Reference number: A2485; UID:92218390; PMID:1313796
A;Accession: A2485
A;Molecule type: DNA
A;Residues: 1-15 <MIA>
A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIN:93780, NCBIP:93787)
R;Kaui, R.K.; Hildebrandt, B.; Roberts, S.; Jagadeeswaran, P.
Gene 41, 311-314, 1986
A;Title: Isolation and characterization of human blood-coagulation factor X cDNA.
A;Reference number: A25853; UID:86221713; PMID:3011603
A;Accession: A25853
A;Molecule type: mRNA
A;Residues: 19-284, 'E', 289-488 <KAU>
A;Cross-references: GB:M22613; NID:g180335; PIDN:AAA51984.1; PID:g180336
R;Fung, M.R.; Hay, C.W.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985
A;Title: Characterization of an almost full-length cDNA coding for human blood coagulat
A;Reference number: A22208; UID:85216545; PMID:2582420
A;Accession: A22208
A;Molecule type: mRNA
A;Residues: 13-441, 'S', 443-488 <FUN>
A;Cross-references: GB:X03194; NID:g182840; PIDN:AAA52490.1; PID:g182841
R;Leytus, S.P.; Chung, D.W.; Kisiel, W.; Kurachi, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984

A>Title: Characterization of a cDNA coding for human factor X.
A:Reference number: A21284; MUID:84222026; PMID:6587384
A:Accession: A21284
A:Molecule type: mRNA
A:Residues: 13-284, 'E', 289-488 <LE2>
A:Cross-references: GB:K01886
R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weiner Biochemistry 22, 2875-2884, 1983
A>Title: Complete amino acid sequence of the light chain of human blood coagulation factor X
A:Reference number: A20362; MUID:8325207; PMID:6871167
A:Accession: A20362
A:Molecule type: protein
A:Residues: 41-179 <MCM>
R:Inoue, K.; Morita, T.
Eur. J. Biochem. 218, 153-163, 1993
A>Title: Identification of O-linked oligosaccharide chains in the activation peptides of factor X
A:Reference number: S39414; MUID:94062825; PMID:8243461
A:Accession: S39415
A:Molecule type: protein
A:Residues: 183-234 <INO>
A>Note: glycosylation sites
A>Note: Identification and characterization of beta-hydroxyaspartic acid
R:Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhushanam, K.; Lyman, G. Gene 84, 517-519, 1989
A>Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human factor X
A:Reference number: I54051; MUID:90128299; PMID:2612918
A:Accession: I54051
A>Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-23 <RES>
A:Cross-references: GB:M33297; NID:G183860; PIDN:AAA52636.1; PID:G553330
R:Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Blass J. Mol. Biol. 232, 947-966, 1993
A>Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
A:Reference number: A49458; MUID:93360277; PMID:8355279
A:Contents: annotation; X-ray crystallography, 2.2 angstroms
C:Comment: The two chains held together by one disulfide bond are formed from a single-cysteine
C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or factor X
C:Genetics:
A:Gene: GDB:F10
A:Cross-references: GDB:I19890; OMIM:227600
A:Map position: 13q34-13q34
A:Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
A>Note: deficiency of this factor causes Stuart disease
C:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of factor V
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-40/Domain: propeptide #status predicted <PRO>
F:25-84/Domain: Gla domain homology <GLA>
F:41-179/Product: coagulation factor X light chain #status experimental <LCH>
F:90-121/Domain: EGF homology <EGI>
F:129-164/Domain: EGF homology <EG2>
F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
F:183-234/Domain: activation peptide #status experimental <APT>
F:235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
F:235-462/Domain: trypsin homology <TRY>
F:46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted
F:57-62/Disulfide bonds: #status predicted
F:100-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:193/Modified site: carboxyglutamate (Thr) (covalent) #status experimental
F:199,211/Binding site: carboxyglutamate (Asn) (covalent) #status experimental
F:221,231/Binding site: carboxyglutamate (Asn) (covalent) #status experimental
F:234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #status predicted
F:276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 53.18; Score 102; DB 1; Length 488;
Best Local Similarity 40.98; Pred. No. 2.9e-09;
Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
QY 1 ANAFLLXLRFGSLXRCXCKXQCSPXXARXIFKDXRKLFWISY 44

Db 41 ANSFLEEMKKGHLRECEMEETCSYEAREVFEDSDKTNFPMKY 84
RESULT 7
EXBO
coagulation factor Xa (BC 3.4.21.6) precursor - bovine
N:Alternate names: Stuart factor
C:Species: Bos primigenius taurus (cattle)
C>Date: 24-Apr-1984 #sequence revision 17-Mar-1987 #text change 09-Jul-2004
C:Accession: A22867; A14997; A12030; A34412; S39414; A00925
R:Fung, M.R.; Campbell, R.M.; MacGillivray, T.A. Nucleic Acids Res. 12, 4481-4492, 1984
A>Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a signal peptide
A:Reference number: A22867; MUID:84247315; PMID:6330671
A:Accession: A22867
A:Molecule type: mRNA
A:Residues: 1-487 <FUN>
A:Cross-references: UNIPROT:P00743; GB:X00673; NID:G192; PIDN:CAA25286.1; PID:G193
R:Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K. Biochemistry 19, 659-667, 1980
A>Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
A:Reference number: A14997; MUID:80130563; PMID:6766735
A:Accession: A14997
A:Molecule type: protein
A:Residues: 41-102, 'N', 104-180 <ENF>
R:McMullen, B.A.; Fujikawa, K.; Kisiel, W. Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factors
A:Reference number: A20274; MUID:83308813; PMID:6688526
A:Contents: annotation; revision to residue 103
R:Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H. Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
A>Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
A:Reference number: A12030; MUID:76053069; PMID:1059093
A:Accession: A12030
A:Molecule type: protein
A:Residues: 183-292, 294-295, 'GDE', 299-334, 336-348, 'AE', 351-354, 356-441, 'GKFG', 446-492 <TJ>
R:Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J. J. Biol. Chem. 264, 16897-16904, 1989
A>Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal factor X
A:Reference number: A34412; MUID:89380326; PMID:2789221
A:Accession: A34412
A:Molecule type: protein
A:Residues: 85-126 <PER>
A>Note: beta-hydroxyaspartic acid site
R:Inoue, K.; Morita, T. Eur. J. Biochem. 218, 153-163, 1993
A>Title: Identification of O-linked oligosaccharide chains in the activation peptides of factor X
A:Reference number: S39414; MUID:94062825; PMID:8243461
A:Accession: S39414
A:Molecule type: protein
A:Residues: 183-196;199-209;216-233 <INO>
A>Note: carboxyglutamate binding sites
R:Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; Davies Biochemistry 11, 4899-4903, 1972
A>Title: Bovine factor X-la (activated Stuart factor). Evidence of homology with mammalian factor X
A:Reference number: A12453; MUID:73053314; PMID:4264286
A:Contents: annotation; active site
R:Fujikawa, K.; Titani, K.; Davies, E.W. Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
A>Title: Activation of bovine factor X (Stuart factor): conversion of factor Xaalpha to factor Xbeta
A:Reference number: A13504; MUID:76053121; PMID:1059122
A:Contents: annotation; activation
R:Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J. J. Biol. Chem. 259, 5705-5710, 1984
A>Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic acid
A:Reference number: A38024; MUID:84185716; PMID:6546930
R:Morita, T.; Jackson, C.M. J. Biol. Chem. 261, 4008-4014, 1986
A:Reference number: A38025; MUID:86140210; PMID:3949800

```
F;43-461/Product: protein C #status predicted <PRC>  
F;91-130/Domain: EGF homology <EG1>  
F;139-174/Domain: EGF homology <EG2>  
P;213-485/Domain: trypsin homology <TRY>  
F;47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status I  
F;112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
F;121-130,139-150,146-159,161-174,182-320,239-255,373-387,398-426/Disulfide bonds: #stat  
F;215,291,355/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;254,300,402/Active site: His, Asp, Ser #status predicted
```

Query Match 52.1%; Score 100; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 6.le-Og;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRPGSLRXKXXQCSFFAXRXPFKDAARTKLFWISY 44
 ||| : |||| |
Db 42 ANSPLEVRAGSLRECMEEICDPFEAQEIFONVEDTLFAFIKY 85
 ||| : |||| |

RESULT 9
EXRT
coagulation factor Xa (EC 3.4.21.6) precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004
C;Accession: S49075; JC4670; PS0190; PS0190; I62745
R;Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
Thromb. Res. 80, 63-73, 1995
A;Title: Evidence for competition between vitamin K-dependent clotting factors for intracel
A;Reference number: A58498; UID:96093366; PMID:8578539
A;Accession: S49075
A;Molecule type: mRNA
A;Residues: 1-482 <STA>
A;Cross-references: UNIPROT:Q63207; EMBL:X79807; NID:G506600; PIDN:CAA56202.1; PID:G506600
A;Note: submitted to the EMBL Data Library, June 1994
A;Note: neither the complete nucleic acid sequence nor the complete translation are show
R;Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
Gene 189, 269-273, 1996
A;Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
A;Reference number: JC4670; UID:96194815; PMID:8647460
A;Accession: JC4670
A;Molecule type: mRNA
A;Residues: 1-482 <STA>
A;Cross-references: EMBL:X79807; NID:G506600; PIDN:CAA56202.1; PID:G506601
A;Experimental source: Cos-1 cell
R;Enryoji, K.; Miyazaki, K.; Kato, H.
J. Biochem. 109, 890-898, 1991
A;Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plas
A;Reference number: PS0190; UID:92041742; PMID:1718949
A;Accession: PS0191
A;Molecule type: protein
A;Residues: 41-58,'X',60-65 <ENJ1>
A;Accession: PS0190
A;Molecule type: protein
A;Residues: 183-186,'X',188-207 <ENJ2>
R;Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
Eur. J. Haematol. 52, 162-168, 1994
A;Title: Analysis of the partial nucleotide sequences and deduced primary structures of t
A;Reference number: I46196; UID:94222160; PMID:8168596
A;Accession: I62745
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 295-383,'G','385-455 <MUR>
A;Cross-references: GB:D21215; NID:g415309; PIDN:BAA04756.1; PID:g455396
C;Function:
A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pres
A;Pathway: blood coagulation
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutami
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-40/Domain: propeptide #status predicted <PRO>
F;25-84/Domain: Gla domain homology <GLA>
F;41-179/Product: coagulation factor X light chain #status predicted <LCH>
F;90-121/Domain: EGF homology <EG1>

F:129-164/Domain: EGF homology <EG2>
 F:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>
 F:183-231/Domain: activation peptide #status predicted <APT>
 F:232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>
 F:232-460/Domain: trypsin homology <TRY>
 F:46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #stat
 F:57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-340,238-243,259-275,388-402,41
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F:187/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:208/Binding site: carbohydrate (Thr) (covalent) #status predicted
 F:219/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:231-232/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat
 F:274,320,417/Active site: His, Asp, Ser #status predicted

Query Match 50.0%; Score 96; DB 1; Length 482;
 Best Local Similarity 40.9%; Pred. No. 3e-08;
 Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLRXKXQCSFXXARXIFKDXRTKLFWISY 44
 DB 41 ANSPFEIKGNLRECVETCSFEAREVFNEDNKTTEFWNKY 84

RESULT 10
 EXCH
 coagulation factor Xa (EC 3.4.21.6) precursor - chicken
 N:Alternate names: virus-activating proteinase
 C:Species: Gallus gallus (chicken)
 C:Date: 12-Feb-1993 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004
 C:Accession: S15838; S20380; S20381
 R:Suzuki, H.; Harada, A.; Hayaashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; Na
 FEBS Lett. 283, 281-285, 1991
 A:Title: Primary structure of the virus activating protease from chick embryo. Its ident
 A:Reference number: S15838; MUID:91257322; PMID:2044767
 A:Accession: S15838
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-475 <SUZ>
 A:Cross-references: UNIPROT:P25155; DBJ:D00844; NID:9222869; PIDN:BAA00724.1; PID:92228
 R:Gotoh, B.; Yamauchi, F.; Ogasawara, T.; Nagai, Y.
 FEBS Lett. 296, 274-278, 1992
 A:Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsib
 A:Reference number: S20380; MUID:92164779; PMID:1537403
 A:Accession: S20380
 A:Molecule type: protein
 A:Residues: 41-55 <G02>
 A:Accession: S20381
 A:Molecule type: protein
 A:Residues: 241-246,'X',248-251,'X',253-261 <G0T>
 C:Function:
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
 A:Pathway: blood coagulation
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-40/Domain: propeptide #status predicted <PRO>
 F:25-84/Domain: Gla domain homology <GLA>
 F:121-185/Product: coagulation factor X light chain #status experimental <LCH>
 F:90-121/Domain: EGF homology <EG1>
 F:129-167/Domain: EGF homology <EG2>
 F:186-475/Product: coagulation factor X heavy chain #status predicted <HCH>
 F:186-240/Domain: activation peptide #status predicted <APT>
 F:241-475/Product: coagulation factor Xa heavy chain #status experimental <AHC>
 F:241-468/Domain: trypsin homology <TRY>
 F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #s
 F:57-62,90-101,95-110,112-121,129-140,136-152,154-167,175-348,247-252,267-283,396-410,42
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F:196,207,228,285/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:282,328,425/Active site: His, Asp, Ser #status predicted

Query Match 47.4%; Score 91; DB 1; Length 475;
 Best Local Similarity 38.6%; Pred. No. 2.1e-07;
 Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLRXKXQCSFXXARXIFKDXRTKLFWISY 44
 DB 41 ANSFLBEMKOGNIERECNEBRCSEAREAFEDNKTTEFWNIY 84

RESULT 11
 KFBO
 coagulation factor IXa (EC 3.4.21.22) precursor - bovine
 N:Alternate names: Christmas factor
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Nov-1980 #sequence revision 03-Aug-1984 #text_change 09-Jul-2004
 C:Accession: A14757; B20274; I45891; A00923
 R:Katayama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.; Tit
 Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979
 A:Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas fac
 A:Reference number: A14757; MUID:80056619; PMID:291916
 A:Accession: A14757
 A:Molecule type: protein
 A:Residues: 1-63,'T',65-416 <KAT>
 A:Cross-references: UNIPROT:P00741
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coa
 A:Reference number: A20274; MUID:83308813; PMID:6688526
 A:Accession: B20274
 A:Molecule type: protein
 A:Residues: 59-63,'X',65-69 <MCM>
 R:Choo, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.
 Nature 299, 178-180, 1982
 A:Title: Molecular cloning of the gene for human anti-haemophilic factor IX.
 A:Reference number: I45891; MUID:82272386; PMID:6287289
 A:Accession: I45891
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 52-139 <CHO>
 A:Cross-references: GB:J00007; NID:G163053; PIDN:AAA30520.1; PID:G163054
 R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, S
 J. Biochem. 104, 867-868, 1988
 A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag
 A:Reference number: A44556; MUID:89213999; PMID:3149637
 A:Contents: annotation
 A:Note: structure and location of a carbohydrate covalently bound to Ser
 C:Comment: Factor IX is activated by factor XIa, which excises the activation peptide pr
 C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K-
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro
 C:Function:
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the preser
 A:Pathway: blood coagulation intrinsic pathway
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
 F:1-146/Product: coagulation factor IXa light chain #status experimental <ALC>
 F:1-45/Domain: Gla domain homology <EG1>
 F:88-124/Domain: EGF homology <EG2>
 F:147-181/Domain: activation peptide #status experimental <APT>
 F:182-416/Product: coagulation factor IXa heavy chain #status experimental <AHC>
 F:182-409/Domain: trypsin homology <TRY>
 F:7,8,15,17,20,21,26,27,30,33,36,40/Modified site: gamma-carboxyglutamic acid (Glu) #stat
 F:18-23,51-62,56-71,73-82,88-99,95-109,111-124,132-290,207-223,337-351,362-390/Disulfide
 F:53/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F:64/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:158,168,173,261/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:222,270,366/Active site: His, Asp, Ser #status predicted

Query Match 44.8%; Score 86; DB 1; Length 416;
 Best Local Similarity 44.1%; Pred. No. 1.3e-06;
 Matches 15; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 11 GSLRXKXQCSFXXARXIFKDXRTKLFWISY 44
 DB 12 GNLERCKBEKCSFEAREVFENTEKTTEFWKOY 45

F;106-111/disulfide bonds: #status predicted
F;110/Binding site: carboxylate (Thr) (covalent) #status absent
F;113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F;139,290,355/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;211-212/cleavage site: Arg-Leu (Chrombin) #status experimental
F;253,299,402/Active site: His, Asp, Ser #status predicted
F;371/Binding site: carbohydrate (Asn) (covalent) #status atypical

Query Match 43.8%; Score 84; DB 1; Length 461;
Best Local Similarity 43.9%; Pred. No. 3.1e-06;
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRPGSLRXCKKQCSPFXAKRIFKDAXRTKLFW 41
||| ||| ||| ||| ||| ||| ||| |||
Db 43 ANSFLELRHSSLRECIIEICDFEEAKEIFQNVDVTLFAW 83

RESULT 13

KFHU

coagulation factor IXA (EC 3.4.21.22) precursor [validated] - human
N;Alternate names: antihemophilic factor B; Christmas factor
C;Species: Homo sapiens (man)
C;Date: 17-Dec-1982 #sequence revision 30-Jun-1987 #text change 09-Jul-2004
C;Accession: A00922; A37570; A30511; A32989; A22673; A21337; A37546; A30623; A60486; A20:
Biochemistry 24, 3736-3750, 1985
R;Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.
A;Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).
A;Reference number: A00922; MUID:86000558; PMID:2994716
A;Accession: A00922
A;Molecule type: DNA
A;Residues: 1-461 <YOS>
A;Cross-references: UNIPROT:P00740; GB:K02402; NID:g182612; PIDN:AAB53620.1; PID:g182613
R;Anson, D.S.; Choo, K.H.; Rees, D.J.G.; Giannelli, F.; Gould, K.; Huddleston, J.A.; Brov
EMBO J. 3, 1053-1060, 1984
A;Title: The gene structure of human anti-haemophilic factor IX.
A;Reference number: A37570; MUID:84236100; PMID:6329734
A;Accession: A37570
A;Molecule type: DNA
A;Residues: 1-461 <ANS>
A;Cross-references: GB:K02048
R;Reitman, P.H.; Bertina, R.M.; Ploos van Amstel, J.K.; Riemsma, A.; Briet, E.
Blood 72, 1074-1076, 1988
A;Title: The putative factor IX gene promoter in hemophilia B Leyden.
A;Reference number: A30511; MUID:88327116; PMID:3416069
A;Accession: A30511
A;Molecule type: DNA
A;Residues: 8-24 <REI>
A;Cross-references: EMBL:X55008; NID:g311288; PIDN:CAB38245.2; PID:g4469253
R;Koerberl, D.D.; Bottema, C.D.K.; Buerstedde, J.M.; Sommer, S.S.
Am. J. Hum. Genet. 45, 448-457, 1989
A;Title: Functionally important regions of the factor IX gene have a low rate of polymor
A;Reference number: A32989; MUID:89371752; PMID:2773937
A;Accession: A32989
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 30-92 <KOE>
R;McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; St
Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985
A;Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulati
A;Reference number: A22673; MUID:85190593; PMID:3857619
A;Accession: A22673
A;Molecule type: mRNA
A;Residues: 1-193, 'T', 195-461 <MCG>
A;Cross-references: GB:M11309; NID:g180552; PIDN:AAA52023.1; PID:g180553
A;Note: the authors translated the codon ACA for residue 29 as Tyr
R;Jaye, M.; de la Salle, H.; Schamber, F.; Balland, A.; Kohli, V.; Findeli, A.; Tolstoshe
Nucleic Acids Res. 11, 2325-2335, 1983
A;Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-ba
A;Reference number: A21337; MUID:83220786; PMID:6687940
A;Accession: A21337
A;Molecule type: mRNA
A;Residues: 1-193, 'T', 195-461 <JAY>
A;Cross-references: GB:J00137; NID:g182610; PIDN:AAA52763.1; PID:g182611

R; Jagadeeswaran, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T. Somat. Cell Mol. Genet. 10, 465-473, 1984

A; Title: Isolation and characterization of human factor IX cDNA: identification of Tag I

A; Reference number: A37546; MUID:84300526; PMID:6089357

A; Accession: A37546

A; Molecule type: mRNA

A; Residues: 38-193, 'T', 195-326 <JAG>

A; Cross-references: GB:M35672

R; Kurachi, K.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982

A; Title: Isolation and characterization of a cDNA coding for human factor IX.

A; Reference number: A30623; MUID:83065193; PMID:6959130

A; Accession: A30623

A; Molecule type: mRNA

A; Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A',

A; Cross-references: GB:J00136; NID:9182608; PIDN:AAA98726.1; PID:9182609

A; Experimental source: liver

R; Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.

Vox Sang. 58, 21-29, 1990

A; Title: Development of an immunoaffinity process for factor IX purification.

A; Reference number: A60486; MUID:90194857; PMID:2316207

A; Accession: A60486

A; Molecule type: protein

A; Residues: 47-52, 'XX', 55-60, 'X', 62, 'XX', 65 <THA>

R; McMullen, B.A.; Fujikawa, K.; Kisiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A; Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co

A; Reference number: A20274; MUID:83308813; PMID:6688526

A; Accession: A20274

A; Molecule type: protein

A; Residues: 105-109, 'X', 111-115 <MCM>

R; Balland, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Sall

Eur. J. Biochem. 172, 565-572, 1988

A; Title: Characterisation of two differently processed forms of human recombinant factor

A; Reference number: S02527; MUID:88166735; PMID:3280312

A; Accession: S02527

A; Molecule type: protein

A; Residues: 29-63 <BAL>

A; Note: processed forms expressed in recombinant system

R; Jallat, S.; Perraud, F.; Dalemans, W.; Balland, A.; Dieterle, A.; Faure, T.; Meulien,

EMBO J. 9, 3295-3301, 1990

A; Title: Characterization of recombinant human Factor IX expressed in transgenic mice an

A; Reference number: S12058; MUID:91006024; PMID:2209546

A; Accession: S12058

A; Molecule type: mRNA; protein

A; Residues: 1-68 <JAL>

A; Note: processed forms expressed in recombinant system

R; Hanford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campbe

EMBO J. 9, 475-480, 1990

A; Title: The first EGF-like domain from human factor IX contains a high-affinity calcium

A; Reference number: S12377; MUID:90151623; PMID:2406129

A; Accession: S12377

A; Molecule type: protein

A; Residues: 92-130 <HAN>

A; Note: NMR detection of calcium binding by domain expressed in recombinant system

R; de la Salle, C.; Charnantier, J.L.; Baas, M.J.; Schwartz, A.; Wiesel, M.L.; Grunebaum,

Thromb. Haemost. 70, 370-371, 1993

A; Title: A deletion located in the 3' non translated part of the factor IX gene responsi

A; Reference number: I59612; MUID:94054330; PMID:8236150

A; Accession: I59612

A; Status: translated

A; Molecule type: DNA

A; Residues: 444-461 <RES>

A; Cross-references: GB:S66752; NID:G439773; PIDN:AAB28588.1; PID:G439774

R; Scofield, E.S.; Koerber, D.D.; Sarkar, G.; Sommer, S.S.

Science 239, 491-494, 1988

A; Title: Genomic amplification with transcript sequencing.

A; Reference number: I59529; MUID:88127096; PMID:3340835

A; Accession: I59529

A; Status: translated

A; Molecule type: DNA

A; Residues: 290-359 <RE2>

A; Cross-references: GB:M19063; NID:G182622; PIDN:AAA52456.1; PID:G182623

R; Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimonishi, Y.; Nishimura, H.; Iwe

Biochemistry 33, 5167-5171, 1994

A; Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically lin

A; Reference number: A54255; MUID:94227047; PMID:8172892

A; Accession: A54255

A; Molecule type: protein

A; Residues: 'D', 204, 'X', 206-211, 'D', 214, 'X', 216-221, 'D' <AGA>

A; Note: the residues designated 'X' were determined to be threonine bound to carbohydrate

R; Di Scipio, R.G.; Kurachi, K.; Davie, E.W.

J. Clin. Invest. 61, 1528-1536, 1978

A; Title: Activation of human factor IX (Christmas factor).

A; Reference number: A18483; MUID:78194509; PMID:659613

A; Contents: annotation; activation; active site; carbohydrate binding

R; McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.

Am. Soc. Hematol. Abstr. 64(Suppl.1), 262a, 1984

A; Reference number: A37569

A; Contents: annotation

A; Note: 194-Thr was also found

R; Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.

J. Biol. Chem. 259, 5698-5704, 1984

A; Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding

A; Reference number: A37543; MUID:84185715; PMID:6425296

A; Contents: annotation; calcium binding

R; Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.

J. Biol. Chem. 260, 2583, 1985

A; Reference number: A37544

A; Contents: annotation; calcium binding, correction

R; Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.

Cell 45, 343-348, 1986

A; Title: Defective propeptide processing of blood clotting factor IX caused by mutation c

A; Reference number: A37545; MUID:86189947; PMID:3009023

A; Contents: annotation; signal sequence cleavage site

R; Suehiro, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya,

J. Biol. Chem. 264, 21257-21265, 1989

A; Title: Blood clotting factor IX B(M) Nagoya: substitution of arginine 180 by tryptophan

A; Reference number: A30622; MUID:90078229; PMID:2592373

A; Contents: annotation; sequence of mutant B(M) Nagoya

A; Note: carboxylation, glycosylation, and cleavage sites

R; Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tee, A.G.D.; Brownlee

submitted to the Brookhaven Protein Data Bank, November 1991

A; Reference number: A51252; PDB:1IXA

A; Contents: annotation; conformation by (1)H-NMR, residues 92-130

A; Note: recombinant form expressed in yeast

C; Comment: Factor IX is activated by factor Xla, which excises the activation peptide pro

C; Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K-

C; Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro

C; Genetics:

A; Gene: GDB:F9

A; Cross-references: GDB:119900; OMIM:306900

A; Map position: Xq27.1-Xq27.2

A; Introns: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1

C; Function:

A; Description: catalyzes the proteolytic activation of coagulation factor X in the preser

A; Pathway: blood coagulation intrinsic pathway

C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C; Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam

F; 1-28/Domain: signal sequence #status predicted <SIG>

F; 29-46/Domain: propeptide #status experimental <PPT>

F; 31-91/Domain: Gla domain homology <GLA>

F; 47-191/Product: coagulation factor IXa light chain #status experimental <ALC>

F; 97-128/Domain: EGF homology <EG1>

F; 134-170/Domain: EGF homology <EG2>

F; 192-226/Domain: activation peptide #status experimental <ACT>

F; 227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>

F; 227-454/Domain: trypsin homology <TRY>

F; 53, 64, 63, 66, 67, 72, 73, 76, 79, 82, 86/Modified site: gamma-carboxyglutamic acid (Glu) #st

F; 64-69, 97-108, 102-117, 119-128, 134-145, 141-155, 157-170, 178-335, 252-268, 382-396, 407-435/Df

F; 99/Binding site: carbohydrate (ser) (covalent) #status experimental

F; 110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F; 191-192/Cleavage site: Arg-Ala (coagulation factor Xla) #status experimental

F; 203, 213/Binding site: carboxylate (Asn) (covalent) #status experimental

F; 205, 217/Binding site: carboxylate (Thr) (covalent) #status experimental

F; 226-227/Cleavage site: Arg-Val (coagulation factor Xla) #status experimental

Query Match 43.2%; Score 83; DB 1; Length 461;
Best Local Similarity 44.1%; Pred. No. 4.6e-06;
Matches 15; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 11 GSLRXCKXQCSFXKXARXKPKDAXRTKLFWISY 44
DB 58 GNLERECHEEKCSFEARVFNTERTEFTFWKQY 91

RESULT 14
TBHU
thrombin (EC 3.4.21.5) precursor [validated] - human
N:Alternate names: coagulation factor II
N:Contents: prothrombin
C:Species: Homo sapiens (man)
C:Date: 30-Nov-1980 #sequence revision 22-Jul-1994 #text_change 09-Jul-2004
A:Accession: A29351; A00914; B00914; A37549; A37550; I51952
R:Degen, S.J.F.; Davie, E.W., 1987
Biochemistry 26, 6165-6177, 1987
A:Title: Nucleotide sequence of the gene for human prothrombin.
A:Reference number: A29351; MUID:88077877; PMID:2825773
A:Accession: A29351
A:Molecule type: DNA
A:Residues: 1-822 <DE>
A:Cross-references: UNIPROT:P00734; GB:M17262; GB:M33691; NID:G558069; PIDN:AAC63054.1;
R:Degen, S.J.F.; MacGillivray, R.T.A.; Davie, E.W.,
Biochemistry 22, 2087-2097, 1983
A:Title: Characterization of the complementary deoxyribonucleic acid and gene coding for
A:Reference number: A00914; MUID:83231469; PMID:6305407
A:Accession: A00914
A:Molecule type: mRNA
A:Residues: 8-163, 'N', 165-622 <DE2>
A:Cross-references: GB:V00595; GB:J00307; PIDN:CAA23842.1; PID:G1335344
A:Accession: B00914
A:Molecule type: DNA
A:Residues: 188-311 <DE3>
R:Walz, D.A.; Hewett-Emmatt, D.; Seegers, W.H.,
Proc. Natl. Acad. Sci. U.S.A. 74, 1969-1972, 1977
J. Biol. Chem. 252, 4942-4957, 1977
A:Title: Primary structure of human prothrombin 2 and alpha-thrombin.
A:Reference number: A37550; MUID:77207112; PMID:873923
A:Accession: A37550
A:Molecule type: protein
A:Residues: 44-118, 'N', 120, 'S', 122-163, 'I', 165-175, 'A', 177-182, 'T', 184-193, 'MV', 196-308,
R:Butkowski, R.J.; Ellison, J.; Downing, M.R.; Mann, K.G.,
J. Biol. Chem. 261, 13210-13215, 1986
A:Reference number: A37551; MUID:87008532; PMID:3759958
A:Contents: annotation; activation cleavages
R:MacGillivray, R.T.; Irwin, D.M.; Guinto, E.R.; Stone, J.C.,
Ann. N.Y. Acad. Sci. 485, 73-79, 1986
A:Title: Recombinant genetic approaches to functional mapping of thrombin.
A:Reference number: I51952; MUID:87182874; PMID:3471151
A:Accession: I51952
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2, 'RI', 5-100 <RES>
A:Cross-references: GB:M33031; NID:G190723; PIDN:AAA60220.1; PID:G190724
C:Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin
C:Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds
C:Comment: can be removed either by factor Xa or thrombin; the cleavage into light and heavy chain
ter 314-Arg, are released in natural blood clotting.
C:Comment: The cleavage after Arg-198, observed in vitro, does not occur in plasma.
C:Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carboxy
ent interaction with the negatively charged phospholipid membrane surface.
C:Comment: The prothrombin precursor is synthesized in the liver.
C:Genetics:
A:Gene: GDB:12

A:Cross-references: GDB:119894; OMIM:176930
A:Map position: lip11-11q12
A:Introns: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552/2
C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C:Keywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; duplicate
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-43/Domain: propeptide #status predicted <PRO>
F:28-87/Domain: Gla domain homology <GLA>
F:44-622/Product: prothrombin #status experimental <MAT>
F:44-327/Domain: activation peptide #status experimental <APT>
F:108-186/Domain: kringle homology <KR1>
F:213-291/Domain: kringle homology <KR2>
F:328-363/Product: thrombin light chain #status experimental <LCH>
F:364-622/Product: thrombin heavy chain #status experimental <HC>
F:364-613/Domain: trypsin homology <TRY>
F:49,50,57,59,62,63,68,69,72,75/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:60-65,90-103,108-186,129-169,157-181,213-291,234-274,262-286/Disulfide bonds: #status
F:121,143/Binding site: carboxylate (Asn) (covalent) #status predicted
F:336-482,536-550,564-594/Disulfide bonds: #status predicted
F:336-482,536-550,564-594/Disulfide bonds: #status experimental
F:391-407/Disulfide bonds: #status predicted
F:406,462/Active site: His, Asp #status predicted
F:416/Binding site: carboxylate (Asn) (covalent) #status experimental
F:568/Active site: Ser #status experimental

Query Match 43.2%; Score 83; DB 1; Length 622;
Best Local Similarity 36.4%; Pred. No. 6e-06;
Matches 16; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

OY 1 ANAPLXXLRPGSLRXKXQCSFXKXARXKPKDAXRTKLFWISY 44
DB 44 ANTFLEVRKGNLERECVEETCSVEEAPALESTATDVFWKY 87

RESULT 15
S10511
thrombin (EC 3.4.21.5) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 09-Jul-2004
C:Accession: S10511; A60576; B42696
R:Dhanich, M.; Monard, D.,
Nucleic Acids Res. 18, 4251, 1990
A:Title: cDNA sequence of rat prothrombin.
A:Reference number: S10511; MUID:90332426; PMID:2377469
A:Accession: S10511
A:Molecule type: mRNA
A:Residues: 1-617 <DIH>
A:Cross-references: UNIPROT:P18292; EMBL:X52835; NID:G56969; PIDN:CAA37017.1; PID:G56970
R:Henrikson, K.P.; Jazin, E.E.; Greenwood, J.A.; Dickerman, H.W.,
Endocrinology 126, 167-175, 1990
A:Title: Prothrombin levels are increased in the estrogen-treated immature rat uterus.
A:Reference number: A60576; MUID:90091942; PMID:2293980
A:Accession: A60576
A:Molecule type: protein
A:Residues: 44-58 <HEN>
A:Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat ute
R:Banfield, D.K.; MacGillivray, R.T.A.,
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
A:Reference number: A42696; MUID:92212913; PMID:1557383
A:Accession: B42696
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 383-617, 'E' <BAN>
A:Cross-references: GB:M81397
C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C:Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydr
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-43/Domain: propeptide #status predicted <PRO>
F:28-88/Domain: Gla domain homology <GLA>
F:44-617/Product: prothrombin #status experimental <PMAT>
F:109-187/Domain: kringle homology <KR1>
F:215-292/Domain: kringle homology <KR2>
F:360-609/Domain: trypsin homology <TRY>

E:50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:61-66,91-104,109-187,130-170,158-182,215-292,236-276
F:402,458-564/Active site: His, Asp, Ser #status predicted
F:61-66,91-104,109-187,130-170,158-182,215-292,236-276,264-287,332-478,387-403,532-546,5

Query Match	41.1%	Score 79;	DB 2;	Length 617;
Best Local Similarity	37.2%	Pred. No. 2.9e05;		
Matches 16;	Conservative	5;	Mismatches 22;	Indels 0;
			Gaps 0;	

Qy	2	NAFLXXLRPGSILXRKCKXXQCFSXXXARXTFKDAXRTKLFWISY	44
	:	: :	
Db	46	SGFLEELRKGNLRECVCEEQQCSYEAAFEALESPOQTDVFWAKY	88

Search completed: August 22, 2005, 09:33:13
Job time : 17 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 22, 2005, 09:19:07 ; Search time 174 Seconds

(without alignments)

129.491 Million cell updates/sec

Title: US-10-031-005-3

Perfect score: 192

Sequence: 1 ANAFLLXLRPGSLRXKCKX.....XXARXIFKDXRTKLFWISY 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	172	89.6	466	1	FA7_HUMAN
2	172	89.6	679	2	Q96PQ8
3	138	71.9	444	1	FA7_RABIT
4	127	66.1	446	1	FA7_MOUSE
5	123	64.1	407	1	FA7_BOVIN
6	114	59.4	459	1	PRTC_PIG
7	109	56.8	460	1	PRTC_MOUSE
8	104	54.2	446	1	FA7_RAT
9	104	54.2	456	1	PRTC_BOVIN
10	102	53.1	443	2	Q8JHC9
11	102	53.1	488	1	FA10_HUMAN
12	101	52.6	425	2	Q8Q4X7
13	101	52.6	492	1	FA10_BOVIN
14	100	52.1	461	1	PRTC_RAT
15	100	52.1	461	2	Q68FY8
16	99	51.6	218	1	TMG1_HUMAN
17	99	51.6	266	2	Q8NEK6
18	99	51.6	433	2	Q8Q4X5
19	98	51.0	490	1	FA10_RABIT
20	96	50.0	482	1	FA10_RAT
21	95	49.5	434	2	Q7T3B6
22	94	49.0	340	2	Q8QY26
23	94	49.0	458	1	PRTC_RABIT
24	94	49.0	469	2	Q9GMD9
25	94	49.0	481	1	FA10_MOUSE
26	93	48.4	456	1	PRTC_CANFA
27	92	47.9	228	2	Q6JPI7
28	92	47.9	229	2	Q8JJ40
29	92	47.9	251	2	Q6DDE6
30	92	47.9	376	1	FA10_TROCA
31	92	47.9	432	2	Q6GNA2

32	91	47.4	475	1	FA10_CHICK	P25155 gallus gall
33	90	46.9	376	1	FA10_HOPST	P83370 hoplocephal
34	90	46.9	524	2	Q7SXH8	Q78xh8 brachydanio
35	89	46.4	179	2	Q8TAS3	Q8tae3 homo sapien
36	89	46.4	198	1	TMG2_MOUSE	Q8r182 mus musculus
37	89	46.4	202	1	TMG2_HUMAN	O14669 homo sapien
38	89	46.4	537	2	Q8Q4X8	Q8Q4w8 fugu rubrip
39	88	45.8	231	1	TMG3_HUMAN	Q9bzd7 homo sapien
40	88	45.8	231	2	Q8N2N6	Q8n2n6 homo sapien
41	88	45.8	250	2	Q6PAQ9	Q6paq9 mus musculus
42	88	45.8	462	2	Q6PAG2	Q6pag2 xenopus lae
43	87.5	45.6	208	2	Q6GPL7	Q6gpl7 xenopus lae
44	87.5	45.6	216	2	Q6DIH4	Q6dih4 xenopus tro
45	87	45.3	442	2	Q8Q4X1	Q8Q4x1 fugu rubrip

ALIGNMENTS

RESULT 1					
FA7_HUMAN					
ID	FA7_HUMAN	STANDARD;	PRT;	466	AA.
AC	P08709; Q14339;				
DT	01-JAN-1988 (Rel. 06, Created)				
DT	01-JAN-1988 (Rel. 06, Last sequence update)				
DT	25-OCT-2004 (Rel. 45, Last annotation update)				
DE	Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator) (SPCA) (Proconvartin) (Eptacog alfa).				
GN	Name=P7;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Liver;				
RX	MEDLINE=86205965; PubMed=3486420;				
RA	Hagen F.S., Gray C.B., O'Hara P.J., Grant P.J., Saari G.C.,				
RA	Woodbury R.G., Hart C.E., Inley M.Y., Kisiel W., Kurachi K.,				
RA	Davie E.W.;				
RT	"Characterization of a cDNA coding for human factor VII.;"				
RL	Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).				
[2]					
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=87260948; PubMed=3037537;				
RA	O'Hara P.J., Grant P.J., Haldeman B.A., Gray C.L., Inley M.Y.,				
RA	Hagen F.S., Murray M.J.;				
RT	"Nucleotide sequence of the gene coding for human factor VII, a				
RT	vitamin K-dependent protein participating in blood coagulation.;"				
RL	Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).				
[3]					
RP	SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.				
RA	Rieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,				
RA	Peel C.L., Toth E.J., Yi O., Nickerson D.A.;				
RT	"SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-				
RT	FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).;"				
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.				
[4]					
RP	SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.				
RX	MEDLINE=9008153; PubMed=3264725;				
RA	Thim L., Bjoern S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,				
RA	Pedersen A.H., Hedner U.;				
RT	"Amino acid sequence and posttranslational modifications of human				
RT	factor VIIa from plasma and transfected baby hamster kidney cells.;"				
RL	Biochemistry 27:7785-7793(1988).				
[5]					
RN	CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.				
RP	MEDLINE=91250411; PubMed=1904059;				
RX	Bjoern S., Foster D.C., Thim L., Wiberg F.C., Christensen M.,				
RA	Komiyama Y., Pedersen A.H., Kisiel W.;				
RT	"Human plasma and recombinant factor VII. Characterization of O-				
RT	glycosylations at serine residues 52 and 60 and effects of site-				
RT	directed mutagenesis of serine 52 to alanine.;"				

RL J. Biol. Chem. 266:11051-11057(1991).
RN [6]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=90062160; PubMed=2511201;
RA Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T., Takao T.,
RA Shimonishi Y., Iwanaga S.;
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide (Xyl2-
RT Glc) O-glycosidically linked to a serine residue in the first
RT epidermal growth factor-like domain of human factors VII and IX and
RT protein Z and bovine protein Z.";
RL J. Biol. Chem. 264:20320-20325(1989).
RN [7]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z.";
RL Adv. Exp. Med. Biol. 281:121-131(1990).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=96175641; PubMed=8598903; DOI=10.1038/380041a0;
RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
RT "The crystal structure of the complex of blood coagulation factor VIIa
RT with soluble tissue factor.";
RL Nature 380:41-46(1996).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=99126536; PubMed=9925787; DOI=10.1006/jmbi.1998.2452;
RA Zhang E., St Charles R., Tulinsky A.;
RT "Structure of extracellular tissue factor complexed with factor VIIa
RT inhibited with a BPTI mutant.";
RL J. Mol. Biol. 285:2089-2104(1999).
RN [10]
RP STRUCTURE BY NMR OF 105-145.
RX MEDLINE=96367502; PubMed=9692950; DOI=10.1021/bi980522f;
RA Muranyi A., Finn B.E., Gippert G.P., Forsen S., Stenflo J.,
RA Drakenberg T.;
RT "Solution structure of the N-terminal EGF-like domain from human
RT factor VII.";
RL Biochemistry 37:10605-10615(1998).
RN [11]
RP VARIANT GLN-364.
RX MEDLINE=91300046; PubMed=20700047;
RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
RA Meade T.W., Tuddenham E.G.D.;
RT "Purification and characterization of factor VII 304-Gln: a variant
RT molecule with reduced activity isolated from a clinically unaffected
RT male.";
RL Blood 78:132-140(1991).
RN [12]
RP VARIANTS GLN-364 AND PHE-370.
RX MEDLINE=92340074; PubMed=1634227;
RA Marchetti G., Patraccchini P., Gemmati D., Derosa V., Pinotti M.,
RA Rodorigo G., Casonato A., Girolani A., Bernardi F.;
RT "Detection of two missense mutations and characterization of a repeat
RT polymorphism in the factor VII gene (F7).";
RL Hum. Genet. 89:497-502(1992).
RN [13]
RP VARIANT TYR-238.
RX MEDLINE=93372811; PubMed=8364544;
RA Marchetti G., Ferrati M., Patraccchini P., Redaelli R., Bernardi F.;
RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms
RT (115His and 333Ser) in the human coagulation factor VII gene.";
RL Hum. Mol. Genet. 2:1055-1056(1993).
RN [14]
RP VARIANTS.
RX MEDLINE=94061028; PubMed=8242057;
RA Takamiya O., Kembali-Cook G., Martin D.M.A., Cooper D.N.,
RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,
RA Tuddenham E.G.D., McVey J.H.;
RT "Detection of missense mutations by single-strand conformational
RT polymorphism (SSCP) analysis in five dysfunctional variants of
RT coagulation factor VII.";
RL Hum. Mol. Genet. 2:1355-1359(1993).
RN [15]
RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.
RX MEDLINE=94284305; PubMed=8204879;
RA Chaing S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
RT "Severe factor VII deficiency caused by mutations abolishing the
RT cleavage site for activation and altering binding to tissue factor.";
RL Blood 83:3524-3535(1994).
RN [16]
RP VARIANT SER-367.
RX PubMed=7860081;
RA Dewald G., Noehne M.M., Ruther K.;
RT "A common Ser/Thr polymorphism in the perforin-homologous region of
RT human complement component C7.";
RL Hum. Hered. 44:301-304(1994).
RN [17]
RP VARIANT VAL-354.
RX MEDLINE=95072589; PubMed=7981691;
RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
RA Rodeghiero F., Marchetti G.;
RT "Topologically equivalent mutations causing dysfunctional coagulation
RT factors VII (294Ala-->Val) and X (334Ser-->Pro).";
RL Hum. Mol. Genet. 3:1175-1177(1994).
RN [18]
RP VARIANT MIE HIS-307.
RX MEDLINE=95064662; PubMed=7974346;
RA Ohiwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S., Suzuki K.;
RT "Factor VII M1e: homozygous asymptomatic type I deficiency caused by
RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
RT catalytic domain.";
RL Thromb. Haemost. 71:773-777(1994).
RN [19]
RP VARIANT MET-419.
RX MEDLINE=96247510; PubMed=8652821;
RA Arbini A.A., Mannucci P.M., Bauer K.A.;
RT "A Thr359Met mutation in factor VII of a patient with a hereditary
RT deficiency causes defective secretion of the molecule.";
RL Blood 87:5085-5094(1996).
RN [20]
RP VARIANTS TRP-283; LYS-325; VAL-358; GLN-364; GLU-402 AND GLN-413.
RX MEDLINE=97001216; PubMed=8844208;
RA DOI=10.1002/(SICI)1098-1004(1996)8:2<108::AID-HUMU2>3.3.CO;2-6;
RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
RA Lunghi B., Rodeghiero F., Marchetti G.;
RT "Mutation pattern in clinically asymptomatic coagulation factor VII
RT deficiency.";
RL Hum. Mutat. 8:108-115(1996).
RN [21]
RP VARIANT VAL-304.
RX MEDLINE=97037613; PubMed=8883260;
RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M., Zaizov R.,
RA Seligsohn U.;
RT "Ala244Val is a common, probably ancient mutation causing factor VII
RT deficiency in Moroccan and Iranian Jews.";
RL Thromb. Haemost. 76:283-291(1996).
RN [22]
RP VARIANT MORIOKA PRO-13.
RX MEDLINE=98235713; PubMed=9576180;
RA Ozawa T., Takikawa Y., Niya K., Ejiri N., Suzuki K., Sato S.,
RA Sakuragawa N.;
RT "Factor VII Moriooka (FVII L-26P): a homozygous missense mutation in
RT the signal sequence identified in a patient with factor VII
RT deficiency.";
RL Br. J. Haematol. 101:47-49(1998).
RN [23]
RP VARIANTS MALTA THR-194 AND VAL-304.
RX MEDLINE=98112461; PubMed=9452082;
RA Alshinawi C., Scerri C., Gaidies R., Aquilina A., Felice A.E.;
RT "Two new missense mutations (P134T and A244V) in the coagulation
RT factor VII gene.";

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RL Hum. Mutat. Suppl. 1:S189-S191(1998).
RN [24]

Query Match      89.6%; Score 172; DB 1; Length 466;
Best Local Similarity 77.3%; Pred. No. 4.3e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ANAFELXLRPGSLRXKCKXQCSFXXARXIFPKDAXRTKLFWISY 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ANAFLEELRPGSLRECKEQCSFEAREIFPKDAERTKLFWISY 104

RESULT 2
ID Q96PQ8 PRELIMINARY; PRT; 679 AA.
AC Q96PQ8;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Factor VII active site mutant immunoconjugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX "NCBI_TaxID=9606;
   [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Hu Z., Garen A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF272774; AAK58686.2; -.
DR HSSP; P08709; 1KLI.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; Trypsin; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLA; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 679 AA; 75552 MW; 0B0023AE70A067A1 CRC64;
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Query Match      89.6%; Score 172; DB 2; Length 679;
Best Local Similarity 77.3%; Pred. No. 6.4e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ANAFELXLRPGSLRXKCKXQCSFXXARXIFPKDAXRTKLFWISY 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 39 ANAFLEELRPGSLRECKEQCSFEAREIFPKDAERTKLFWISY 82

RESULT 3
ID FA7_RABIT STANDARD; PRT; 444 AA.
AC P98I39; P79224;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
GN Name=F7;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
   [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation
RT factor VII.";
RL Thromb. Res. Suppl. 69:231-238 (1993).
RN [2]
RP REVISION TO 395.
RL TISSUE=Liver;
RA Ruiz S.R., Blajchman M.A., Clarke B.J.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Initiates the extrinsic pathway of blood coagulation.
CC Serine protease that circulates in the blood in a zymogen form.
CC Factor VII is converted to factor VIIa by factor Xa, factor XIIa,
CC factor IXa, or thrombin by minor proteolysis. In the presence of
CC tissue factor and calcium ions, factor VIIa then converts factor X
CC to factor Xa by limited proteolysis. Factor VIIa will also convert
CC factor IX to factor IXa in the presence of tissue factor and
CC calcium (By similarity).
CC -!- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -!- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by
CC a disulfide bond (By similarity).
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some
CC glutamate residues allows the modified protein to bind calcium (By
CC similarity).
CC -!- SIMILARITY: Belongs to the peptidase S1 family.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
CC domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; U77477; AAB37326.1; -.
CC HSSP; P08709; 1FAK.
CC MEROPS; S01.215; -.
CC InterPro; IPR000152; Asx_hydroxyl_S.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR001438; EGF_11.
DR
```

InterPro; IPR006209; EGF like.
 InterPro; IPR002383; GLA_blood.
 InterPro; IPR001254; Peptidase_S1.
 InterPro; IPR001314; Peptidase_S1A.
 InterPro; IPR009003; Pept_Ser_Cys.
 InterPro; IPR000294; VitK_dep_GLA.
 Pfam; PF00008; EGF; 2.
 Pfam; PF00594; GLA; 1.
 Pfam; PF00089; Trypsin; 1.
 PRINTS; PR00722; CHYMOTRYPSIN.
 PRINTS; PR00010; EGFBLD.
 PRINTS; PR00001; GLABLOOD.
 SMART; SM00179; EGF_CA; 1.
 SMART; SM00069; GLA; 1.
 SMART; SM00020; Tryp_Spc; 1.
 PROSITE; PS00010; ASX_HYDROXYL; 1.
 PROSITE; PS00022; EGF_1; 1.
 PROSITE; PS01186; EGF_2; 1.
 PROSITE; PS00026; EGF_3; 1.
 PROSITE; PS01187; EGF_CA; 1.
 PROSITE; PS00011; GLA_1; 1.
 PROSITE; PS00998; GLA_2; 1.
 PROSITE; PS00240; TRYPSIN_DOM; 1.
 PROSITE; PS00134; TRYPSIN_HIS; 1.
 PROSITE; PS00135; TRYPSIN_SER; 1.
 Blood coagulation; Calcium-binding; EGF-like domain;
 Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;
 Plasma; Repeat; Serine protease; Signal; Vitamin K; Zymogen.
 SIGNAL 1 21 Potential.
 PROPEP 22 39 Potential.
 CHAIN 40 191 Factor VII light chain.
 CHAIN 192 444 Factor VII heavy chain.
 DOMAIN 40 84 GLA.
 DOMAIN 85 121 EGF-like 1, calcium-binding (Potential).
 DOMAIN 126 167 EGF-like 2.
 DOMAIN 192 444 Serine protease.
 SITE 191 192 Cleavage (by factor Xa, factor XIIa, factor IXa, or thrombin) (By similarity).
 ACT_SITE 232 232 By similarity.
 ACT_SITE 281 281 By similarity.
 ACT_SITE 383 383 By similarity.
 BINDING 377 377 Substrate (By similarity).
 DISULFID 56 61 By similarity.
 DISULFID 89 100 By similarity.
 DISULFID 94 109 By similarity.
 DISULFID 111 120 By similarity.
 DISULFID 130 141 By similarity.
 DISULFID 137 151 By similarity.
 DISULFID 153 166 By similarity.
 DISULFID 174 301 By similarity.
 DISULFID 198 203 By similarity.
 DISULFID 217 233 By similarity.
 DISULFID 349 368 By similarity.
 DISULFID 379 407 By similarity.
 MOD_RES 45 45 4-carboxyglutamate.
 MOD_RES 46 46 4-carboxyglutamate.
 MOD_RES 53 53 4-carboxyglutamate.
 MOD_RES 55 55 4-carboxyglutamate.
 MOD_RES 58 58 4-carboxyglutamate.
 MOD_RES 59 59 4-carboxyglutamate.
 MOD_RES 64 64 4-carboxyglutamate.
 MOD_RES 65 65 4-carboxyglutamate.
 MOD_RES 68 68 4-carboxyglutamate.
 MOD_RES 74 74 4-carboxyglutamate.
 MOD_RES 102 102 3-hydroxyaspartate (By similarity).
 CARBOHYD 211 211 N-linked (GlcNAc...) (Potential).
 CARBOHYD 242 242 N-linked (GlcNAc...) (Potential).
 CARBOHYD 306 306 N-linked (GlcNAc...) (Potential).
 SEQUENCE 444 AA; 49011 MW; 0481ABC4FE5427F8 CRC64;

Query Match 71.9%; Score 138; DB 1; Length 444;
 Best Local Similarity 59.1%; Pred. No. 5.6e-16;
 Matches 26; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLRXKXQXQCSFXAXRIFKDXRTKLFWSY 44
 DB 40 ANSFLELRPGSLRECKBELCSFEAREVFQSTERTKQFWITY 83
 RESULT 4
 FA7_MOUSE
 ID FA7_MOUSE STANDARD; PRT; 446 AA.
 AC P70375; Q61109;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
 DE Names: P7; Synonyms: Ccf7;
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96276538; PubMed=8701412;
 RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D., Castellino F.J.;
 RT "Characterization of a cDNA encoding murine coagulation factor VII.";
 RL Thromb. Haemost. 75:481-487 (1996).
 [2]
 RP SEQUENCE FROM N.A.
 RN MEDLINE=97127167; PubMed=8972017;
 RA Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
 RT "Nucleotide structure and characterization of the murine blood coagulation factor VII gene.";
 RL Thromb. Haemost. 76:957-964 (1996).
 CC -1- FUNCTION: Initiates the extrinsic pathway of blood coagulation. Serine protease that circulates in the blood in a zymogen form. Factor VII is converted to factor VIIa by factor Xa, factor XIIa, factor IXa, or thrombin by minor proteolysis. In the presence of tissue factor and calcium ions, factor VIIa then converts factor X to factor Xa by limited proteolysis. Factor VIIa will also convert factor IX to factor IXa in the presence of tissue factor and calcium (By similarity).
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor Xa.
 CC -1- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by a disulfide bond (By similarity).
 CC -1- TISSUE SPECIFICITY: Plasma.
 CC -1- PTM: The vitamin K-dependent, enzymatic carboxylation of some glutamate residues allows the modified protein to bind calcium (By similarity).
 CC -1- SIMILARITY: Belongs to the peptidase S1 family.
 CC -1- SIMILARITY: Contains 2 EGF-like domains.
 CC -1- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla) domain.

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 CC EMBL; U44795; AAC25570.1; -;
 CC EMBL; U66079; AAC33796.1; -;
 CC HSSP; P08709; 1BF9.
 CC MEROPS; S01.215; -;
 CC MGD; MGI:109325; F7.
 CC InterPro; IPR000152; Asx_hydroxyl_S.
 CC InterPro; IPR000742; EGF_2.
 CC InterPro; IPR001881; EGF_Ca.
 CC InterPro; IPR001438; EGF_I1.


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DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBLLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00089; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00998; GLA_2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Calcium-binding; Direct protein sequencing;
KW EGF-like domain; Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase;
KW Plasma; Repeat; Serine protease; Vitamin K; Zymogen.
FT CHAIN 1 152 Factor VII light chain.
FT CHAIN 153 407 Factor VII heavy chain.
FT DOMAIN 1 45 Gla.
FT DOMAIN 46 82 EGF-like 1, calcium-binding (Potential).
FT DOMAIN 87 128 EGF-like 2.
FT DOMAIN 153 407 Serine protease.
FT SITE 152 153 Cleavage (by factor Xa, factor XIIIa, factor IXa, or thrombin).
FT ACT_SITE 193 193 By similarity.
FT ACT_SITE 242 242 By similarity.
FT BINDING 338 338 Substrate (By similarity).
FT DISULFID 17 22 By similarity.
FT DISULFID 50 61 By similarity.
FT DISULFID 55 70 By similarity.
FT DISULFID 72 81 By similarity.
FT DISULFID 91 102 By similarity.
FT DISULFID 98 112 By similarity.
FT DISULFID 114 127 By similarity.
FT DISULFID 135 262 By similarity.
FT DISULFID 159 164 By similarity.
FT DISULFID 178 194 By similarity.
FT DISULFID 310 329 By similarity.
FT DISULFID 340 368 By similarity.
FT MOD_RES 6 6 4-carboxyglutamate.
FT MOD_RES 7 7 4-carboxyglutamate.
FT MOD_RES 14 14 4-carboxyglutamate.
FT MOD_RES 16 16 4-carboxyglutamate.
FT MOD_RES 19 19 4-carboxyglutamate.
FT MOD_RES 20 20 4-carboxyglutamate.
FT MOD_RES 25 25 4-carboxyglutamate.
FT MOD_RES 26 26 4-carboxyglutamate.
FT MOD_RES 29 29 4-carboxyglutamate.
FT MOD_RES 35 35 4-carboxyglutamate.
FT CARBOHYD 52 52 O-linked (Glc...).
FT CARBOHYD 145 145 N-linked (GlcNAc...).
FT CARBOHYD 203 203 N-linked (GlcNAc...).
SQ SEQUENCE 407 AA; 44431 MW; 703E1FE0636F7F10 CRC64;
Query Match 64.1%; Score 123; DB 1; Length 407;
Best Local Similarity 52.3%; Pred. No. 2.6e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
Oy 1 ANAFLLXLPGLRXCCKXQCSPFXARXIFKDXRTRKLFWSY 44
| | | | | | | | | | | | | | | | | | | | |
Db 1 ANGFEELLFGLRERCREELCSFEAHEIFRNEERTQFWVS 44
| | | | | | | | | | | | | | | | | | | | |

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RESULT 6
PRTC_PIG STANDARD; PRT; 459 AA.
AC QSGLP2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Vitamin K-dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolytic IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).
DE Names:PROC;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21121490; PubMed=11229814;
RA Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J., Kim H.K.W.;
RA "Porcine factor V: cDNA cloning, gene mapping, three-dimensional protein modeling of membrane binding sites and comparative anatomy of domains.";
RT Cell. Mol. Life Sci. 58:148-159(2001).
CC -|- FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa in the presence of calcium ions and phospholipids.
CC -|- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIIa.
CC -|- SUBUNIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin.
CC -|- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -|- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.
CC -|- MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain. This GLA-independent binding site is necessary for the recognition of the thrombin-thrombomodulin complex.
CC -|- SIMILARITY: Belongs to the peptidase S1 family.
CC -|- SIMILARITY: Contains 2 EGF-like domains.
CC -|- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla) domain.
-----
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EMBL; AF191307; AAG28380.1; -.
HSSP; P04070; 1AUT.
MEROPS; S01.218; -.
InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF_like.
InterPro; IPR002383; GLA_blood.
InterPro; IPR006210; IEGF.
InterPro; IPR009003; Pept_Ser_Cys.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PF00008; EGF; 2.
Pfam; PF00594; Gla; 1.
PRINTS; PR00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.

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DR PRINTS; PRO0001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYP SPC; 1.
DR PROSITE; PS00010; ASX HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF CA; 1.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00998; GLA_2; 1.
DR PROSITE; PS00240; TRYPSIN DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Calcium-binding; EGF-like domain;
KW Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;
KW Repeat; Serine protease; Signal; Vitamin K.
FT SIGNAL 1 18
FT PROPEP 19 41
FT CHAIN 42 459
FT CHAIN 42 196
FT CHAIN 199 459
FT PEPTIDE 199 213
FT SITE 213 214
FT DOMAIN 42 87
FT DOMAIN 96 131
FT DOMAIN 135 175
FT DOMAIN 214 459
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 55 55
FT MOD_RES 57 57
FT MOD_RES 60 60
FT MOD_RES 61 61
FT MOD_RES 66 66
FT MOD_RES 67 67
FT MOD_RES 70 70
FT MOD_RES 112 112
FT ACT_SITE 225 225
FT ACT_SITE 301 301
FT ACT_SITE 400 400
FT DISULFID 58 63
FT DISULFID 91 110
FT DISULFID 100 105
FT DISULFID 104 119
FT DISULFID 121 130
FT DISULFID 139 150
FT DISULFID 146 159
FT DISULFID 161 174
FT DISULFID 182 321
FT DISULFID 240 385
FT DISULFID 371 385
FT CARBOHYD 138 138
FT CARBOHYD 292 292
FT CARBOHYD 353 353
SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;

Query Match 59.4%; Score 114; DB 1; Length 459;
Best Local Similarity 50.0%; Pred. No. 1.3e-11;
Matches 22; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLRXKCKXQCSEXXARXIFKDXRTKLFWISY 44
DB 42 ANSFLEELRPSLSRECKEETCDFEAREIFONTMFWISKY 85

RESULT 7
PRTC_MOUSE
ID PRTC_MOUSE STANDARD; PRT; 460 AA.
AC P33567; O35498; Q91WN8; Q99PC6;

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DT 01-FEB-1994 (Rel. 28, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Vitamin K-dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolytic IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).
DE Name=Proc;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALEB/C; TISSUE=Liver;
RX MEDLINE=92316897; PubMed=1618739;
RA Tada N., Sato M., Teujimura A., Iwase R., Hashimoto-Gotoh T.;
RT "Isolation and characterization of a mouse protein cDNA.";
RL J. Biochem. 111:491-495(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=98152576; PubMed=9493582;
RA Jalbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,
Castellino F.J.;
RT "Nucleotide structure and characterization of the murine gene encoding anticoagulant protein C.";
RL Thromb. Haemost. 79:310-316(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Korf I.;
RT "Complete sequence of UC72A01.";
RN Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=12477932; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 274-433 FROM N.A.
RC STRAIN=BALEB/C;
RX MEDLINE=94318474; PubMed=8043441;
RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
RT "A comparative study of partial primary structures of the catalytic region of mammalian protein C.";
RL Br. J. Haematol. 86:590-600(1994).
CC -!- FUNCTION: Protein C is a vitamin K-dependent serine protease that
CC regulates blood coagulation by inactivating factors Va and VIIIa
CC in the presence of calcium ions and phospholipids.
CC -!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIa.
CC -!- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
CC into a light chain and a heavy chain held together by a disulfide
CC bond. The enzyme is then activated by thrombin, which cleaves a

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tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombospondin.

-!- TISSUE SPECIFICITY: Plasma; synthesized in the liver.

-!- PM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.

-!- MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain. This GLA-independent binding site is necessary for the recognition of the thrombin-thrombospondin complex.

-!- SIMILARITY: Belongs to the peptidase S1 family.

-!- SIMILARITY: Contains 2 EGF-like domains.

-!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (GLA) domain.

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EMBL; D10445; BAA01235.1; -.

EMBL; AF034569; AAC33795.1; -.

EMBL; AF318182; AAK07918.1; -.

EMBL; BC013896; AAH13896.1; -.

EMBL; D43755; BAA07812.1; -.

PIR; JX0210; JX0210.

HSSP; P04070; LAUT.

MEROPS; S01.218; -.

MGD; MGI:97771; PROC.

InterPro; IPR000152; Asx hydroxyl_s.

InterPro; IPR000742; EGF_2.

InterPro; IPR001881; EGF_Ca.

InterPro; IPR006209; EGF_Like.

InterPro; IPR002383; GLA blood.

InterPro; IPR009003; Pept Ser Cys.

InterPro; IPR001254; PeptIdase_S1.

InterPro; IPR001314; Peptidase_S1A.

InterPro; IPR000294; VitK_dep_GLA.

Pfam; PF00008; EGF; 2.

Pfam; PF00594; Gla; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

PRINTS; PR00001; GLABLOOD.

SMART; SM00179; EGF_CA; 1.

SMART; SM00069; GLA; 1.

SMART; SM00020; TRY_SPC; 1.

PROSITE; PS00010; ASX_HYDROXYL; 1.

PROSITE; PS00022; EGF_1; 1.

PROSITE; PS01186; EGF_2; 2.

PROSITE; PS00026; EGF_3; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS00011; GLA_1; 1.

PROSITE; PS00998; GLA_2; 1.

PROSITE; PS02040; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00133; TRYPSIN_SER; 1.

Blood coagulation; Calcium-binding; EGF-like domain;

Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;

Repeat; Serine protease; Signal; Vitamin K.

SIGNAL; 1 33 By similarity.

PROPEP 34 41 By similarity.

CHAIN 42 460 Vitamin K-dependent protein C.

CHAIN 42 196 Vitamin K-dependent protein C light chain

CHAIN 199 460 (By similarity).

CHAIN 199 460 (By similarity).

PEPTIDE 199 212 Activation peptide (By similarity).

SITE 212 213 Cleavage (by thrombin) (By similarity).

DOMAIN 42 87 Gla.

DOMAIN 96 131 EGF-like 1.

FT DOMAIN 135 175 EGF-like 2.

FT DOMAIN 213 460 Serine protease.

FT MOD_RES 47 47 4-carboxyglutamate (By similarity).

FT MOD_RES 48 47 4-carboxyglutamate (By similarity).

FT MOD_RES 55 55 4-carboxyglutamate (By similarity).

FT MOD_RES 57 57 4-carboxyglutamate (By similarity).

FT MOD_RES 60 60 4-carboxyglutamate (By similarity).

FT MOD_RES 61 61 4-carboxyglutamate (By similarity).

FT MOD_RES 66 66 4-carboxyglutamate (By similarity).

FT MOD_RES 67 67 4-carboxyglutamate (By similarity).

FT MOD_RES 70 70 4-carboxyglutamate (By similarity).

FT MOD_RES 112 112 3-hydroxyaspartate (By similarity).

FT ACT_SITE 253 253 Charge relay system.

FT ACT_SITE 299 299 Charge relay system.

FT ACT_SITE 401 401 Charge relay system.

FT DISULFID 58 63 By similarity.

FT DISULFID 91 110 By similarity.

FT DISULFID 100 105 By similarity.

FT DISULFID 104 119 By similarity.

FT DISULFID 121 130 By similarity.

FT DISULFID 139 150 By similarity.

FT DISULFID 146 159 By similarity.

FT DISULFID 161 174 By similarity.

FT DISULFID 182 319 Interchain (By similarity).

FT DISULFID 238 254 By similarity.

FT DISULFID 372 386 By similarity.

FT CARBOHYD 214 214 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 290 290 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 354 354 N-linked (GlcNAc...) (Potential).

FT VARIANT 327 327 Q -> QQ (in strain BALB/c).

FT VARIANT 392 392 D -> N (in strain BALB/c).

FT CONFLICT 65 65 F -> L (in Ref. 3).

FT SEQUENCE 460 AA; 51818 MW; 0117F26568FCC274 CRC64;

Query Match 56.8%; Score 109; DB 1; Length 460;

Best Local Similarity 47.7%; Pred. No. 1e-10;

Matches 21; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLXRYCKXQCSFXXARXIFKDXRTKLFWSY 44

DB 42 ANSFLEMRPGSLRECEMEECDFEBAQEIFQNVEDTLAFWKY 85

RESULT 8

FA7_RAT

ID FA7_RAT STANDARD; PRT; 446 AA.

AC Q8K3U6;

DT 05-JUL-2004 (Rel. 44, Created)

DT 05-JUL-2004 (Rel. 44, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin

DE conversion accelerator).

GN Name=F7;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley;

RA Murphy K., Ramaker M.,

RT "Nucleotide sequence of the cDNA encoding rat coagulation factor

VII";

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Initiates the extrinsic pathway of blood coagulation.

CC Serine protease that circulates in the blood in a zymogen form.

CC Factor VII is converted to factor VIIa by factor Xa, factor XIIa,

CC factor IXa, or thrombin by minor proteolysis. In the presence of

CC tissue factor and calcium ions, factor VIIa then converts factor X

CC to factor Xa by limited proteolysis. Factor VIIa will also convert

CC factor IX to factor IXa in the presence of tissue factor and

CC calcium (By similarity).

RT "Amino acid sequence of the heavy chain of bovine protein C.";

RL J. Biol. Chem. 257:12180-12190(1982).

RN [5]

RP PROCESSING, AND CALCIUM-BINDING DATA.

RX MEDLINE=83213513; PubMed=6304092;

RA Esmon N.L.; Debault L.E.; Esmon C.T.;

RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-

RT domainless protein C.";

RL J. Biol. Chem. 258:5548-5553(1983).

RN [6]

RP PROCESSING, AND CALCIUM-BINDING DATA.

RX MEDLINE=83213514; PubMed=6406503;

RA Johnson A.E.; Esmon N.L.; Laue T.M.; Esmon C.T.;

RT "Structural changes required for activation of protein C are induced

RT by Ca²⁺ binding to a high affinity site that does not contain gamma-

RT carboxyglutamic acid.";

RL J. Biol. Chem. 258:5548-5553(1983).

CC -1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved

CC into a light chain and a heavy chain held together by a disulfide

CC bond. The enzyme is then activated by thrombin, which cleaves a

CC tetradecapeptide from the amino end of the heavy chain; this

CC reaction, which occurs at the surface of endothelial cells, is

CC strongly promoted by thrombomodulin.

CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.

CC -1- PM: The vitamin K-dependent, enzymatic carboxylation of some Glu

CC residues allows the modified protein to bind calcium.

CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to

CC another site, beyond the GLA domain. This GLA-independent binding

CC site is necessary for the recognition of the thrombin-

CC thrombomodulin complex.

CC -1- SIMILARITY: Belongs to the peptidase S1 family.

CC -1- SIMILARITY: Contains 2 EGF-like domains.

CC -1- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)

CC domain.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; K02435; AAA30685.1; -.

DR PIR; A26250; KXBO.

DR HSSP; P04070; 1AUT.

DR MEROPS; S01.218; -.

DR InterPro; IPR000152; Asx hydroxyl_S.

DR InterPro; IPR000742; EGF_2.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR006209; EGF_like.

DR InterPro; IPR002383; GLA_blood.

DR InterPro; IPR006210; IEGF.

DR InterPro; IPR009003; Pept_Ser_Cys.

DR InterPro; IPR001254; Peptidase_S1.

DR InterPro; IPR001314; Peptidase_S1A.

DR InterPro; IPR000294; VitK_dep_GLA.

DR Pfam; PF00008; EGF; 2.

DR Pfam; PF00594; Gla; 1.

DR Pfam; PF00089; Trypsin; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00001; GLABLOOD.

DR SMART; SM00181; EGF; 2.

DR SMART; SM00069; GLA; 1.

DR SMART; SM00020; Tryp_Spc; 1.

DR PROSITE; PS00010; ASX_HYDROXYL; 1.

DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS50026; EGF_3; 1.

DR PROSITE; PS01187; EGF_CA; 1.

DR PROSITE; PS00011; GLA_1; 1.

DR PROSITE; PS50998; GLA_2; 1.

DR PROSITE; PS50240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

KW Blood coagulation; Calcium-binding; Direct protein sequencing;

KW EGF-like domain; Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase;

KW Hydroxylation; Repeat; Serine protease; Signal; Vitamin K.

KW NON_TER 1

FT SIGNAL <1 29

FT PROPEP 30 39

FT CHAIN 40 456

FT CHAIN 40 194

FT CHAIN 197 456

FT PEPTIDE 197 210

FT DOMAIN 40 85

FT DOMAIN 94 129

FT DOMAIN 133 173

FT DOMAIN 211 456

FT MOD_RES 45 45

FT MOD_RES 46 46

FT MOD_RES 53 53

FT MOD_RES 55 55

FT MOD_RES 58 58

FT MOD_RES 59 59

FT MOD_RES 62 62

FT MOD_RES 64 64

FT MOD_RES 65 65

FT MOD_RES 68 68

FT MOD_RES 74 74

FT MOD_RES 110 110

FT ACT_SITE 252 252

FT ACT_SITE 298 298

FT ACT_SITE 397 397

FT DISULFID 56 61

FT DISULFID 89 108

FT DISULFID 98 103

FT DISULFID 102 117

FT DISULFID 119 128

FT DISULFID 137 148

FT DISULFID 144 157

FT DISULFID 159 172

FT DISULFID 180 318

FT DISULFID 237 253

FT DISULFID 368 382

FT DISULFID 393 421

FT CARBOHYD 136 136

FT CARBOHYD 289 289

FT CARBOHYD 350 350

FT CARBOHYD 366 366

FT VARIANT 82 82

FT CONFLICT 455 456

FT CONFLICT 51407 MM; CAA6F833F894C209 CRC64;

SQ SEQUENCE 456 AA; 51407 MM; CAA6F833F894C209 CRC64;

Query Match 54.2%; Score 104; DB 1; Length 456;

Best Local Similarity 45.5%; Pred. No. 8e-10;

Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANAFLLXLRPGSLXRXCKXQCSFXXARXIFKDXRTKLFWSY 44

DB 40 ANSFLEELAPGNVERECSEVCEFEAREIFQNTEDTMAFWSFY 83

RESULT 10

Q8JHC9 PRELIMINARY; PRT; 443 AA.

AC Q8JHC9; (TRENBLrel. 22, Created)

DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Coagulation factor VIII.
GN Name=f71;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Hanumanthiah R., Day K., Jagadeeswaran P.;
RT "Comprehensive analysis of blood coagulation pathways in Teleostei:
RT Evolution of coagulation factor genes and identification of zebrafish
RT factor VIII.";
RL Blood Cells Mol. Dis. 0:0-0(2002).
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL: AF519546; RAM88142.1; -;
DR EMBL: AF515269; AAN71000.1; -;
DR HSSP: P00740; ICFH.
DR ZFIN: ZDB-GENE-021206-10; f71.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0004263; F:chymotrypsin activity; IEA.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004295; F:trypsin activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR000742; EGF 2.
DR InterPro: IPR006209; EGF like.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR001254; Peptidase S1.
DR InterPro: IPR001314; Peptidase S1A.
DR InterPro: IPR009003; Pept Ser Cys.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF 1.
DR Pfam: PF00594; Gla; 1.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PRO0722; CHYMOTRYPSIN.
DR PRINTS: PRO0001; GLABLOOD.
DR SMART: SM00181; EGF 2.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00022; EGF 1; UNKNOWN_1.
DR PROSITE: PS01186; EGF 2; 2.
DR PROSITE: PS00026; EGF 3; 1.
DR PROSITE: PS00011; GLA 1; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR EGF-like domain; Hydrolase; Protease; Serine protease.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 443 AA; 48823 MW; 2D2504718AE94FF4 CRC64;
Query Match 53.1%; Score 102; DB 2; Length 443;
Best Local Similarity 41.9%; Pred. No. 1.8e-09;
Matches 18; Conservative 8; Mismatches 1; Indels 0; Gaps 0;
QY 2 NAFLLXRLPGSLKRXCKXQCSFXXARXIFKDXRTKLFWSY 44
DB 40 SGFLEMKAGNLERECVEIEICDYEARVEFDDRTKQFWLSY 82
RESULT 11
ID FA10 HUMAN STANDARD; PRT; 488 AA.
AC P00742; Q14340;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor)
DE Prower factor).
GN Name=F10;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91216473; PubMed=1902434; DOI=10.1016/0378-1119(91)90141-W;
RA Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
RT human coagulation factor X.";
RL Gene 99:291-294(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87026500; PubMed=3768336;
RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
RT "Gene for human factor X: a blood coagulation factor whose gene
RT organization is essentially identical with that of factor IX and
RT protein C.";
RL Biochemistry 25:5098-5102(1986).
RN [3]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Ozuna M., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RT "SeattlesNPs. NHLBI HL66682 program for genomic applications, UW-
RT PHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (APR-2002) to the ENBL/GenBank/DBSJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Maiz M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 13-488 FROM N.A.
RX MEDLINE=85216545; PubMed=2582420;
RA Fung M.R., Hay C.W., McGillivray R.T.A.;
RT "Characterization of an almost full-length cDNA coding for human blood
RT coagulation factor X.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
RN [6]
RP SEQUENCE OF 19-488 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86221713; PubMed=3011603; DOI=10.1016/0378-1119(86)90112-5;
RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
RT "Isolation and characterization of human blood-coagulation factor X
RT cDNA.";
RL Gene 41:311-314(1986).
RN [7]
RP SEQUENCE OF 41-179.
RX MEDLINE=83257207; PubMed=6871167;
RA McMullen B.A., Fujikawa K., Kisiel W., Sasagawa T., Howald W.N.,
RA Kwa E.Y., Weinstein B.;
RT "Complete amino acid sequence of the light chain of human blood
RT coagulation factor X: evidence for identification of residue 63 as
RT beta-hydroxyaspartic acid.";
RL Biochemistry 22:2875-2884(1983).
RN [8]

-1- SIMILARITY: Contains 1 EGF-like domain.

CC EMBL; AF465268; AA033363.1; -.
DR HSP; P08709; 1KLJ.
DR MEROPS; S01.215; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0003802; F:coagulation factor VIIa activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR00152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF II.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR006210; LEGF.
DR InterPro; IPR001254; Peptidase SI.
DR InterPro; IPR001314; Peptidase SLA.
DR InterPro; IPR009003; Rept Ser Cys.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM0069; GLA; 1.
DR SMART; SM00020; TrYP_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF CA; 1.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 425 AA; 47626 MW; 36A69BFD8C6BDAC CRC64;

Query Match 52.6%; Score 101; DB 2; Length 425;
Best Local Similarity 45.5%; Pred. No. 2.6e+09;
Matches 20; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

Qy

1 ANAFLLXRPGSLRXCXXXQCFFXXRXIFPKDXRTKFWISY 44
||| : | | | | | ||| : | | | | | |||
41 ANSFEEIKGLPERECIEEKCSFEAREIYRDERTKEFWHTY 84

RESULT 13

FA10_BOVIN STANDARD; PRT; 492 AA.
ID FA10_BOVIN STANDARD; PRT; 492 AA.
AC P00743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 23-JAN-2005 (Rel. 46, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN Name:F10;
GC Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxId=9913;
RN [1]
RS SEQUENCE OF 1-487 FROM N.A.
RP MEDLINE=84247315; PubMed=6330671;
RA Fung M.R., Campbell R.M., McGillivray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain containing a prepro leader sequence."
RL Nucleic Acids Res. 12:4481-4492(1984).

[2] SEQUENCE OF 41-180.
RP MEDLINE=80130563; PubMed=6766735;
RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H., Titani K.;
RA "Amino acid sequence of the light chain of bovine factor XI (Stuart factor).";
RL Biochemistry 19:659-667(1980).
[3] REVISION TO 103.
RP MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kisiel W.;
RA "The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
[4] SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RP MEDLINE=76053069; PubMed=1059093;
RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A., Neurath H.;
RA "Bovine factor XI (Stuart factor): amino-acid sequence of heavy chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
[5] SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
RP MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RA "Identification of O-linked oligosaccharide chains in the activation peptides of blood coagulation factor X. The role of the carbohydrate moieties in the activation of factor X.";
RL Eur. J. Biochem. 218:153-163(1993).
[6] ACTIVE SITE.
RP MEDLINE=73053314; PubMed=4264286;
RA Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A., Neurath H., Davie E.W.;
RA "Bovine factor X la (activated Stuart factor). Evidence of homology with mammalian serine proteases.";
RL Biochemistry 11:4899-4903(1972).
[7] PROCESSING
RP MEDLINE=76053121; PubMed=1059122;
RA Fujikawa K., Titani K., Davie E.W.;
RA "Activation of bovine factor X (Stuart factor): conversion of factor Xa-alpha to factor Xa-beta.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
[8] CALCIUM-BINDING DATA.
RP MEDLINE=84185716; PubMed=6546930;
RA Sugito T., Björk I., Holmgren A., Stenflo J.;
RA "Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic acid-containing region.";
RL J. Biol. Chem. 259:5705-5710(1984).
[9] SULFATION.
RP MEDLINE=86140210; PubMed=3949800;
RA Morita T., Jackson C.M.;
RA "Localization of the structural difference between bovine blood coagulation factors XI and XII to tyrosine 18 in the activation peptide.";
RL J. Biol. Chem. 261:4008-4014(1986).
[10] STRUCTURE BY NMR OF 85-126.
RP MEDLINE=91084483; PubMed=2261466;
RA Selander M., Persson E., Stenflo J., Drakenberg T.;
RA "1H NMR assignment and secondary structure of the Ca2(+)-free form of the amino-terminal epidermal growth factor like domain in coagulation factor X.";
RL Biochemistry 29:8111-8118(1990).
[11] STRUCTURE BY NMR OF 85-126.
RP MEDLINE=92329412; PubMed=1627540;
RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,

CC into a light chain and a heavy chain held together by a disulfide
 CC bond. The enzyme is then activated by thrombin, which cleaves a
 CC tetradecapeptide from the amino end of the heavy chain; this
 CC reaction, which occurs at the surface of endothelial cells, is
 CC strongly promoted by thrombomodulin.
 CC -!- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
 CC residues allows the modified protein to bind calcium.
 CC -!- MISCELLANEOUS: Calcium also binds, with stronger affinity to
 CC another site, beyond the GLA domain. This GLA-independent binding
 CC site is necessary for the recognition of the thrombin-
 CC thrombomodulin complex.
 CC -!- SIMILARITY: Belongs to the peptidase S1 family.
 CC -!- SIMILARITY: Contains 2 EGF-like domains.
 CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
 CC domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X64336; CAA45617.1; -.
 DR PIR; S18994; S18994.
 DR HSSP; P04070; LAUT.
 DR MEROPS; S01.218; -.
 DR RGD; 3411; PROC
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF CA.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR009003; Pept_ser_Cys.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF CA; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRYD_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS01187; EGF CA; 1.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS00998; GLA_2; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Calcium-binding; EGF-like domain;
 KW Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;
 KW Repeat; Serine protease; Signal; Vitamin K.
 FT SIGNAL 1 32 By similarity.
 FT PROPEP 33 41 Vitamin K-dependent protein C.
 FT CHAIN 42 461 Vitamin K-dependent protein C light chain
 FT CHAIN 42 196 (By similarity).
 FT CHAIN 199 461 Vitamin K-dependent protein C heavy chain
 FT CHAIN 199 212 Activation peptide (By similarity).
 FT DOMAIN 42 87 Gla.
 FT DOMAIN 96 131 EGF-like 1.
 FT DOMAIN 135 175 EGF-like 2.
 FT DOMAIN 213 461 Serine protease.
 FT SITE 212 213 Cleavage (by thrombin) (By similarity).

FT MOD_RES 47 47 4-carboxyglutamate (By similarity).
 FT MOD_RES 48 48 4-carboxyglutamate (By similarity).
 FT MOD_RES 55 55 4-carboxyglutamate (By similarity).
 FT MOD_RES 57 57 4-carboxyglutamate (By similarity).
 FT MOD_RES 60 60 4-carboxyglutamate (By similarity).
 FT MOD_RES 61 61 4-carboxyglutamate (By similarity).
 FT MOD_RES 66 66 4-carboxyglutamate (By similarity).
 FT MOD_RES 67 67 4-carboxyglutamate (By similarity).
 FT MOD_RES 70 70 4-carboxyglutamate (By similarity).
 FT MOD_RES 112 112 3-hydroxyaspartate (By similarity).
 FT ACT_SITE 254 254 Charge relay system.
 FT ACT_SITE 300 300 Charge relay system.
 FT ACT_SITE 402 402 Charge relay system.
 FT DISULFID 58 63 By similarity.
 FT DISULFID 91 110 By similarity.
 FT DISULFID 100 105 By similarity.
 FT DISULFID 104 119 By similarity.
 FT DISULFID 121 130 By similarity.
 FT DISULFID 139 150 By similarity.
 FT DISULFID 146 159 By similarity.
 FT DISULFID 161 174 By similarity.
 FT DISULFID 182 320 Interchain (By similarity).
 FT DISULFID 239 255 By similarity.
 FT DISULFID 373 387 By similarity.
 FT DISULFID 398 426 By similarity.
 FT CARBOHYD 215 215 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 291 291 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 355 355 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 461 AA; 51912 MW; 8A4CF93664EDACD5 CRC64;

Query Match 52.1%; Score 100; DB 1; Length 461;

Best Local Similarity 45.5%; Pred. No. 4.3e-09;

Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRPGSLRXKCKXCSPXXARXIPKDXRTKLFWSY 44

Db 42 ANSPLEVRAGSLRECHMEICDFEEAQEIFQNVEDTLAFWKY 85

RESULT 15

Q68FY8

ID Q68FY8 PRELIMINARY; PRT; 461 AA.

AC Q68FY8;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Protein C.

GN Name:Proc.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RC SEQUENCE FROM N.A.

RP TISSUE=Lung;

RX PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Stalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]

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RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Director MGC Project;
RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RL -1_ SMILIARITY; Belongs to peptidase family S1.
DR EMBL; BC078879; AAH78879.1; --
DR InterPro; IPR000152; ASX_HYDROXYL_S.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR PRINTS; PRO0001; GLABLOPSIN.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00179; EGF CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF; 2.
DR PROSITE; PS01187; EGF CA; 1.
DR PROSITE; PS00011; GLA_1; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1_
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Protease; Serine protease.
KW SEQUENCE 461 AA; 51926 MW; C0181CED046B584B CRC64;

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Query Match 52.1%; Score 100; DB 2; Length 461;
Best Local Similarity 45.5%; Pred. No. 4.3e-09;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

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Qy .      1 ANAFLLXLRPGSLRXRCXXXQCSEFXXARXIFKDAXRTKLFWISY 44
          |||::|:||||||| | | | | | | | | | | | | | | | | | |
Db       42 ANSFLEEVRAAGSLERECMEEICDFEAAQEIQFQNVEDTLAFWKY 85
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Search completed: August 22, 2005, 09:36:14
Job time : 176 secs

Result No.	Score	Query		DB	ID	Description
		Match	%			
1	172	89.6	44	3	US-08-955-636-3	Sequence 3, Appli
2	172	89.6	44	4	US-09-302-239-3	Sequence 3, Appli
3	172	89.6	44	4	US-09-497-591-3	Sequence 3, Appli
4	172	89.6	44	4	US-09-803-810-3	Sequence 3, Appli
5	172	89.6	406	1	US-08-293-778-24	Sequence 24, Appli
6	172	89.6	406	1	US-08-295-411-5	Sequence 5, Appli
7	172	89.6	406	2	US-08-955-471-5	Sequence 5, Appli
8	172	89.6	406	4	US-09-782-587B-1	Sequence 1, Appli
9	172	89.6	406	4	US-09-782-587B-3	Sequence 3, Appli
10	172	89.6	406	5	PCT-US92-10242-5	Sequence 5, Appli
11	172	89.6	444	1	US-08-475-845-2	Sequence 2, Appli
12	172	89.6	444	2	US-08-327-690-2	Sequence 2, Appli
13	172	89.6	444	2	US-08-660-289-2	Sequence 2, Appli
14	172	89.6	444	2	US-08-537-807-2	Sequence 2, Appli
15	172	89.6	444	2	US-08-871-003-2	Sequence 2, Appli
16	172	89.6	444	3	US-08-464-233-2	Sequence 2, Appli
17	172	89.6	444	3	US-09-189-607-2	Sequence 2, Appli
18	172	89.6	444	3	US-09-378-907-2	Sequence 2, Appli
19	172	89.6	444	5	PCT-US94-05779-2	Sequence 2, Appli
20	172	89.6	461	4	US-09-949-016-8839	Sequence 8839, Ap
21	172	89.6	466	1	US-07-682-202A-4	Sequence 4, Appli
22	172	89.6	466	1	US-08-021-615A-4	Sequence 4, Appli
23	172	89.6	466	1	US-08-321-777-4	Sequence 4, Appli
24	172	89.6	466	3	US-09-009-217-14	Sequence 14, Appl
25	172	89.6	466	3	US-09-009-656-14	Sequence 14, Appl
26	172	89.6	466	5	PCT-US93-04493-4	Sequence 4, Appli
27	172	89.6	483	4	US-09-949-016-9523	Sequence 9523, Ap

; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-09-302-239-3

Query Match 89.6%; Score 172; DB 4; Length 44;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRPGSLXRCXKXQCSFXXARXIFKDAKRTKLFWISY 44
Db 1 ANAFLLXLRPGSLXRCXKXQCSFXXARXIFKDAKRTKLFWISY 44

RESULT 3
US-09-497-591-3
; Sequence 3, Application US/09497591
; Patent No. 6747003
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary L.
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531-016001
; CURRENT APPLICATION NUMBER: US/09/497,591
; CURRENT FILING DATE: 2000-02-03
; EARLIER APPLICATION NUMBER: 09/302,239
; EARLIER FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: 08/955,636
; EARLIER FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-09-497-591-3

Query Match 89.6%; Score 172; DB 4; Length 44;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRPGSLXRCXKXQCSFXXARXIFKDAKRTKLFWISY 44
Db 1 ANAFLLXLRPGSLXRCXKXQCSFXXARXIFKDAKRTKLFWISY 44

RESULT 4
US-09-803-810-3
; Sequence 3, Application US/09803810
; Patent No. 6762286
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary L.
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/09/803,810
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-09-803-810-3

Query Match 89.6%; Score 172; DB 4; Length 44;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRPGSLXRCXKXQCSFXXARXIFKDAKRTKLFWISY 44
Db 1 ANAFLLXLRPGSLXRCXKXQCSFXXARXIFKDAKRTKLFWISY 44

RESULT 5
US-08-293-778-24
; Sequence 24, Application US/08293778
; Patent No. 5580560
; GENERAL INFORMATION:
; APPLICANT: Nicolaisen, Else M.
; APPLICANT: Bjorn, Soren E.
; APPLICANT: Wiberg, Finn C.
; APPLICANT: Woodbury, Richard
; TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,778
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/104,509
; FILING DATE:
; APPLICATION NUMBER: DK 3235/87
; FILING DATE: 25-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/434,149
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK88/00103
; FILING DATE: 24-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,248
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Agria, Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 3129.224-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-293-778-24

Query Match 89.6%; Score 172; DB 1; Length 406;
Best Local Similarity 77.3%; Pred. No. 1e-20;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRPGSLXRCXKXQCSFXXARXIFKDAKRTKLFWISY 44
Db 1 ANAFLLXLRPGSLXRCXKXQCSFXXARXIFKDAKRTKLFWISY 44

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RESULT 6
US-08-295-411-5
; Sequence 5, Application US/08295411
; Patent No. 5679639
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,411
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
; US-08-295-411-5

Query Match 89.6%; Score 172; DB 1; Length 406;
Best Local Similarity 77.3%; Pred. No. 1e-20;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLXRXCKXQCSFXXARXIFKDAKRTKLFWISY 44
Db 1 ANAFLEELRPGSLERECKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 7
US-08-955-471-5
; Sequence 5, Application US/08955471
; Patent No. 5968751
; GENERAL INFORMATION:
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; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,471
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/295,411
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
; US-08-955-471-5

Query Match 89.6%; Score 172; DB 2; Length 406;
Best Local Similarity 77.3%; Pred. No. 1e-20;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLXRXCKXQCSFXXARXIFKDAKRTKLFWISY 44
Db 1 ANAFLEELRPGSLERECKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 8
US-09-782-587B-1
; Sequence 1, Application US/09782587B
; Patent No. 6806063
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUD
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26
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;; PRIOR APPLICATION NUMBER: PA 2000 00218
;; PRIOR FILING DATE: 2000-02-11
;; PRIOR APPLICATION NUMBER: 60/184,036
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: 60/241,916
;; PRIOR FILING DATE: 2000-10-18
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)-(7)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (14)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (16)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (19)-(20)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (25)-(26)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (29)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (35)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; US-09-782-587B-1

Query Match 89.6%; Score 172; DB 4; Length 406;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRPGSLRXKXKXQCSFXXARXIFKDAERTKLFWISY 44
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Db 1 ANAFLLXLRPGSLRXKXKXQCSFXXARXIFKDAERTKLFWISY 44
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RESULT 9
US-09-782-587B-3
; Sequence 3, Application US/09782587B
; Patent No. 6806063
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUD
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782.587B
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-782-587B-3

Query Match 89.6%; Score 172; DB 4; Length 406;
Best Local Similarity 77.3%; Pred. No. 1e-20;

Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 1 ANAFLLXLRPGSLRXKXKXQCSFXXARXIFKDAERTKLFWISY 44
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Db 1 ANAFLELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 44
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RESULT 10
PCT-US92-10242-5
; Sequence 5, Application PC/TUS9210242
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Meesters, Rolf
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 North Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10242
; FILING DATE: 19921118
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRO472P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
; PCT-US92-10242-5

Query Match 89.6%; Score 172; DB 5; Length 406;
Best Local Similarity 77.3%; Pred. No. 1e-20;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRPGSLRXKXKXQCSFXXARXIFKDAERTKLFWISY 44
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Db 1 ANAFLELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 44
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RESULT 11
US-08-475-845-2

; Sequence 2, Application US/08475845
; Patent No. 5788965

; GENERAL INFORMATION:

; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus

; TITLE OF INVENTION: Modified Factor VII

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 94105-1492

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/475,845

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/327,690

; FILING DATE: 24-OCT-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/065,725

; FILING DATE: 21-MAY-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/662,920

; FILING DATE: 28-FEB-1991

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Parmelee, Steven W.

; REGISTRATION NUMBER: 31,990

; REFERENCES/DOCKET NUMBER: 13952-8-4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-467-9600

; TELEFAX: 415-543-5043

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 444 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-475-845-2

Query Match 89.6%; Score 172; DB 1; Length 444;

Best Local Similarity 77.3%; Pred. No. 1.1e-20;

Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLRXKXQCSFXAXRIFKDAERTKLFWISY 44

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Db 39 ANAFLEELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 12

US-08-327-690-2

; Sequence 2, Application US/08327690

; Patent No. 5817788

; GENERAL INFORMATION:

; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla

; APPLICANT: Bregengaard, Claus

; TITLE OF INVENTION: Modified Factor VII

; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 94105-1492

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/327,690

; FILING DATE: 24-OCT-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/065,725

; FILING DATE: 21-MAY-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/662,920

; FILING DATE: 28-FEB-1991

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Parmelee, Steven W.

; REGISTRATION NUMBER: 31,990

; REFERENCES/DOCKET NUMBER: 13952-8-3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-467-9600

; TELEFAX: 415-543-5043

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 444 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-327-690-2

Query Match 89.6%; Score 172; DB 2; Length 444;

Best Local Similarity 77.3%; Pred. No. 1.1e-20;

Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Db 39 ANAFLEELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 13

US-08-660-289-2

; Sequence 2, Application US/08660289

; Patent No. 5833982

; GENERAL INFORMATION:

; APPLICANT: Berkner, Kathleen L.

; APPLICANT: Petersen, Lars C.

; APPLICANT: Hart, Charles E.

; APPLICANT: Hedner, Ulla

; APPLICANT: Bregengaard, Claus

; TITLE OF INVENTION: Modified Factor VII

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Kourie and Crew

; STREET: One Market Plaza, Steuart Street Tower

; CITY: San Francisco

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 94105-1492

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.24

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; APPLICATION NUMBER: US/08/660,289
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/475,845
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/327,690
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-660-289-2

Query Match      89.6%; Score 172; DB 2; Length 444;
Best Local Similarity 77.3%; Pred. No. 1.1e-20; Indels 0; Gaps 0;
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Db 39 ANAFLELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 14
US-08-537-807-2
; Sequence 2, Application US/08537807
; Patent No. 5861374
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,807
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05779
; FILING DATE: 23-MAY-1994
; APPLICATION NUMBER: US 08/065,725
; FILING DATE: 21-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/662,920
; FILING DATE: 28-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-1PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-537-807-2

Query Match      89.6%; Score 172; DB 2; Length 444;
Best Local Similarity 77.3%; Pred. No. 1.1e-20; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 10;

Qy 1 ANAFLLRLPGSLRXCKXQCSCFXXARXIFKDAERTKLFWISY 44
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Db 39 ANAFLELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 15
US-08-871-003-2
; Sequence 2, Application US/08871003
; Patent No. 5997864
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hedner, Ulla
; APPLICANT: Rasmussen, Mirella E.
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,003
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 90-07C7
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-871-003-2

Query Match      89.6%; Score 172; DB 2; Length 444;
Best Local Similarity 77.3%; Pred. No. 1.1e-20; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 10;

Qy 1 ANAFLLRLPGSLRXCKXQCSCFXXARXIFKDAERTKLFWISY 44
    ||||| ||||| || ||||| ||||| ||||| ||||| |||||
Db 39 ANAFLELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

Search completed: August 22, 2005, 09:37:01
Job time : 44 secs
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	1	172	89.6	44	9	US-09-803-810-3	Sequence 3, Appli
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	3	172	89.6	44	16	US-10-855-068-3	Sequence 3, Appli
	4	172	89.6	406	10	US-09-782-587B-1	Sequence 1, Appli
	5	172	89.6	406	10	US-09-782-587B-3	Sequence 3, Appli
	6	172	89.6	406	14	US-10-109-498-1	Sequence 1, Appli
	7	172	89.6	406	14	US-10-255-032-1	Sequence 1, Appli
	8	172	89.6	406	14	US-10-281-727-1	Sequence 1, Appli
	9	172	89.6	406	15	US-10-386-898-7	Sequence 7, Appli
	10	172	89.6	406	15	US-10-383-898-1	Sequence 1, Appli
	11	172	89.6	406	15	US-10-617-500-1	Sequence 1, Appli

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; Sequence 3, Application US/10298330
; Publication No. US20030100506A1
; GENERAL INFORMATION:
; APPLICANT: Nelisestuen, Gary L.
; TITLE OF INVENTION: Modified Vitamin K-Dependent
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 09531-127001
; CURRENT APPLICATION NUMBER: US/10/298,330
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/497,591
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/302,239
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 08/955,636
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 35
; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid or glutamic acid
US-10-298-330-3

Query Match      89.6%; Score 172; DB 14; Length 44;
Best Local Similarity 100.0%; Pred. No. 5.7e-22;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLXLRPGSLRXCKXQCSPXXARXIFKDXARTKLFWISY 44
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Db 1 ANAFLXLRPGSLRXCKXQCSPXXARXIFKDXARTKLFWISY 44

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US-10-855-068-3
; Sequence 3, Application US/10855068
; Publication No. US20040220106A1
; GENERAL INFORMATION:
; APPLICANT: Nelisestuen, Gary L.
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/10/855,068
; CURRENT FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: US/09/302,239
; PRIOR FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-10-855-068-3

Query Match      89.6%; Score 172; DB 16; Length 44;
Best Local Similarity 100.0%; Pred. No. 5.7e-22;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLXLRPGSLRXCKXQCSPXXARXIFKDXARTKLFWISY 44
   |||||
Db 1 ANAFLXLRPGSLRXCKXQCSPXXARXIFKDXARTKLFWISY 44

RESULT 4
US-09-782-587B-1
; Sequence 1, Application US/09782587B
```

```
; Publication No. US20030096338A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (6)..(7)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD RES
; LOCATION: (14)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD RES
; LOCATION: (16)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD RES
; LOCATION: (19)..(20)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD RES
; LOCATION: (25)..(26)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD RES
; LOCATION: (29)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD RES
; LOCATION: (35)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
US-09-782-587B-1

Query Match      89.6%; Score 172; DB 10; Length 406;
Best Local Similarity 100.0%; Pred. No. 5.3e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLXLRPGSLRXCKXQCSPXXARXIFKDXARTKLFWISY 44
   |||||
Db 1 ANAFLXLRPGSLRXCKXQCSPXXARXIFKDXARTKLFWISY 44

RESULT 5
US-09-782-587B-3
; Sequence 3, Application US/09782587B
; Publication No. US20030096338A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
```



```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-587B-3

Query Match      89.6%; Score 172; DB 10; Length 406;
Best Local Similarity 77.3%; Pred. No. 5.3e-21;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ANAFLXLRPGSLRXCKXQCXFXARXIFKDXARTKLFWISY 44
Db 1 ANAFLEELRPGSLRECKEQSFARXIFKDXARTKLFWISY 44

RESULT 6
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286.200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match      89.6%; Score 172; DB 14; Length 406;
Best Local Similarity 100.0%; Pred. No. 5.3e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLXLRPGSLRXCKXQCXFXARXIFKDXARTKLFWISY 44
Db 1 ANAFLXLRPGSLRXCKXQCXFXARXIFKDXARTKLFWISY 44

RESULT 7
US-10-255-032-1
; Sequence 1, Application US/10255032
; Publication No. US20030100075A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030100075A1o No. US20030100075Aldisk A/S
; TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
; FILE REFERENCE: 6357-WO
; CURRENT APPLICATION NUMBER: US/10/255,032
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: DK PA 2001 01413
; PRIOR FILING DATE: 2001-09-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: human coagulation Factor VII
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate)
```

```
US-10-255-032-1

Query Match      89.6%; Score 172; DB 14; Length 406;
Best Local Similarity 100.0%; Pred. No. 5.3e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLXLRPGSLRXCKXQCXFXARXIFKDXARTKLFWISY 44
Db 1 ANAFLXLRPGSLRXCKXQCXFXARXIFKDXARTKLFWISY 44

RESULT 8
US-10-281-727-1
; Sequence 1, Application US/10281727
; Publication No. US20030130191A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Human Coagulation Factor VII
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 6410.200-US
; CURRENT APPLICATION NUMBER: US/10/281,727
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PA 2001 01627
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 60/335,383
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid
; OTHER INFORMATION: (gamma-carboxyglutamate)
US-10-281-727-1

Query Match      89.6%; Score 172; DB 14; Length 406;
Best Local Similarity 100.0%; Pred. No. 5.3e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLXLRPGSLRXCKXQCXFXARXIFKDXARTKLFWISY 44
Db 1 ANAFLXLRPGSLRXCKXQCXFXARXIFKDXARTKLFWISY 44

RESULT 9
US-10-386-898-7
; Sequence 7, Application US/10386898
; Publication No. US20030229018A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030229018A1o No. US20030229018Aldisk Pharmaceuticals, Inc.
; APPLICANT: Kjalke, Marianne
; APPLICANT: Jakobsen, Palle
; APPLICANT: Stennicke, Henning Ralf
; TITLE OF INVENTION: DIMERIC TF ANTAGONIST
; FILE REFERENCE: 6445.200-US
; CURRENT APPLICATION NUMBER: US/10/386,898
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: Danish Application PA 2002 00373
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US 60/365,935
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 406
; TYPE: PRT
; ORGANISM: human coagulation Factor VII
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)...(406)
```



```
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(406)
; OTHER INFORMATION: Xaa=4-carboxyglutamic acid (gamma-carboxyglutamate)
US-10-617-619-1
```

```
Query Match      89.6%; Score 172; DB 16; Length 406;
Best Local Similarity 100.0%; Pred. No. 5.3e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLXLLRPGSLRXKCKXQCXSFXXARXIFKDAARTKLFWISY 44
   |||||||||||||||||||||||||||||||||||||||||||
Db 1 ANAFLXLLRPGSLRXKCKXQCXSFXXARXIFKDAARTKLFWISY 44
```

RESULT 14

```
US-10-701-294-1
; Sequence 1, Application US/10701294
; Publication NO. US20040143099A1
; GENERAL INFORMATION:
; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
; APPLICANT: Petersen, Lars C
; APPLICANT: Back, Jakob M
; APPLICANT: Meyer, Christian
; TITLE OF INVENTION: Pharmaceutical Composition Comprising a Tissue Factor Antagonist
; TITLE OF INVENTION: and a Blood Glucose Regulator
; FILE REFERENCE: 6608.200-US
; CURRENT APPLICATION NUMBER: US/10/701,294
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: US 60/434,904
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01710
; PRIOR FILING DATE: 2002-11-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: human coagulation Factor VII
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(406)
; OTHER INFORMATION: Xaa=4-carboxyglutamic acid (gamma-carboxyglutamate)
US-10-701-294-1
```

```
Query Match      89.6%; Score 172; DB 16; Length 406;
Best Local Similarity 100.0%; Pred. No. 5.3e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLXLLRPGSLRXKCKXQCXSFXXARXIFKDAARTKLFWISY 44
   |||||||||||||||||||||||||||||||||||||||||||
Db 1 ANAFLXLLRPGSLRXKCKXQCXSFXXARXIFKDAARTKLFWISY 44
```

RESULT 15

```
US-10-669-537-1
; Sequence 1, Application US/10669537
; Publication NO. US20040192602A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; APPLICANT: Olsen, Ole Hvilsted
; TITLE OF INVENTION: Human Coagulation Factor VII Polypeptides
; FILE REFERENCE: 6544.200-US
; CURRENT APPLICATION NUMBER: US/10/669,537
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01423
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 60/417,927
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 13
```

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(406)
; OTHER INFORMATION: Xaa=carboxyglutamic acid (gamma-carboxyglutamate)
US-10-669-537-1
```

```
Query Match      89.6%; Score 172; DB 16; Length 406;
Best Local Similarity 100.0%; Pred. No. 5.3e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLXLLRPGSLRXKCKXQCXSFXXARXIFKDAARTKLFWISY 44
   |||||||||||||||||||||||||||||||||||||||||||
Db 1 ANAFLXLLRPGSLRXKCKXQCXSFXXARXIFKDAARTKLFWISY 44
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Search completed: August 22, 2005, 09:55:12
Job time : 160 secs

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Result No.	Score	Query Match	Length	DB	ID	Description	
1	161.5	81.6	44	2	AAV18305	Human fac	
2	161.5	81.6	44	4	AAB36395	Human fac	
3	161.5	81.6	44	7	ADDS0096	Human vit	
4	161.5	81.6	44	8	ADQ26902	Human vit	
5	161.5	81.6	401	4	AAB84870	Mutant bl	
6	161.5	81.6	401	4	AAB84871	Mutant bl	
7	161.5	81.6	406	2	AAK35764	Factor VI	
8	161.5	81.6	406	2	AAW14510	Modified	
9	161.5	81.6	406	2	AAW14509	Modified	
10	161.5	81.6	406	4	AAU77745	Human fac	
11	161.5	81.6	406	4	AAB84867	Mutant bl	
12	161.5	81.6	406	4	AAB84868	Mutant bl	
13	161.5	81.6	406	4	AAB84869	Mutant bl	
14	161.5	81.6	406	4	AAB84866	Wild-type	
15	161.5	81.6	406	4	AAW52193	Human FVI	
16	161.5	81.6	406	4	AAW52172	Mammalian	
17	161.5	81.6	406	4	AAW52186	Human FVI	
18	161.5	81.6	406	4	AAW52171	Human FVI	
19	161.5	81.6	406	4	AAW52187	Human FVI	
20	161.5	81.6	406	4	AAW52181	Human FVI	
21	161.5	81.6	406	4	AAW52185	Human FVI	
22	161.5	81.6	406	4	AAW52184	Human FVI	
23	161.5	81.6	406	4	AAW52182	Human FVI	
24	161.5	81.6	406	5	AAU77196	Human coa	
25	161.5	81.6	406	5	AAU77191	Human coa	

```
Query Match      81.6%; Score 161.5; DB 2; Length 44;
Best Local Similarity 97.8%; Pred. No. 6.1e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLXRCXKXQCXSFXXARXIFKDXRTKLFWISY 45
   ||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1 ANA-FLXXLRPGSLXRCXKXQCXSFXXARXIFKDXRTKLFWISY 44

RESULT 2
AAB36395
ID AAB36395 standard; peptide; 44 AA.
AC AAB36395;
XX
XX
DT 27-FEB-2001 (first entry)
XX
DE Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
XX
KW Vitamin K-dependent protein; factor VII; protein C; GLA domain;
KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
KW factor X; prothrombin; enhanced membrane binding affinity;
KW clot formation; thrombolytic; haemostatic; bleeding disorder; thrombosis;
KW clotting disorder; haemophilia A; haemophilia B; liver disease.
XX
XX Homo sapiens.
OS
XX WO200066753-A2.
FN
XX 09-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US011416.
PF
XX 29-APR-1999; 99US-00302239.
PR
XX (MINU ) UNIV MINNESOTA.
PA
XX
XX Nelsestuen GL;
PI
XX WPI; 2001-007226/01.
XX
XX Novel vitamin K-dependent polypeptide useful for treating clotting
PT disorders such as thrombosis and hemophilia, comprises modified gamma-
PT carboxy glutamic acid domain that enhances membrane binding affinity.
XX
XX Disclosure; Page 12; 81pp; English.
XX
XX The present invention describes a vitamin K-dependent polypeptide (I)
CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having at
CC least one amino acid substitution, that enhances membrane binding
CC affinity and the activity of the polypeptide relative to a corresponding
CC native vitamin K-dependent polypeptide and inhibits clot formation. (I)
CC can have thrombolytic and haemostatic activities, and can be used as an
CC inhibitor of clot formation. (II) is useful for decreasing clot formation
CC in a mammal, a factor VII or factor IX containing a modified GLA domain
CC is useful for increasing clot formation and for treating a bleeding
CC disorder, including thrombosis and clotting disorders such as haemophilia
CC A, haemophilia B and liver disease. The present sequence represents a
CC wild type human factor VII GLA domain sequence, given in the
CC exemplification of the present invention
XX
XX Sequence 44 AA;
SQ

Query Match      81.6%; Score 161.5; DB 4; Length 44;
Best Local Similarity 97.8%; Pred. No. 6.1e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLXRCXKXQCXSFXXARXIFKDXRTKLFWISY 45
   ||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1 ANA-FLXXLRPGSLXRCXKXQCXSFXXARXIFKDXRTKLFWISY 44
```

```
RESULT 3
ADD50096
ID ADD50096 standard; protein; 44 AA.
XX
XX ADD50096;
AC
XX 15-JAN-2004 (first entry)
XX
XX Human vitamin K-dependent protein #2.
DE
XX Human; vitamin K-dependent protein; gamma-carboxyglutamic acid domain;
XX GLA domain; membrane binding affinity; clot formation; haemophilia;
XX clotting disorder; site directed mutagenesis; haemostatic; anticoagulant;
XX thrombolytic.
XX
XX Homo sapiens.
OS
XX US2003100506-A1.
FN
XX 29-MAY-2003.
XX
XX 18-NOV-2002; 2002US-00298330.
XX
XX 23-OCT-1997; 97US-00955636.
PR
XX 29-APR-1999; 99US-00302239.
PR
XX 03-FEB-2000; 2000US-00497591.
PR
XX (NELS/) NELSESTUEN G L.
PA
XX Nelsestuen GL;
XX
XX WPI; 2003-606646/57.
XX
XX New vitamin K-dependent polypeptide for modulating clot formation in
PT mammals comprises a modified gamma-carboxyglutamic acid domain that
PT enhances membrane binding affinity and activity of the polypeptide.
XX
XX Example 5; SEQ ID NO 3; 51pp; English.
XX
XX The invention relates to a vitamin K-dependent polypeptide comprising a
CC modified gamma-carboxyglutamic acid (GLA) domain that enhances membrane
CC binding affinity and activity of the polypeptide relative to a
CC corresponding native vitamin K-dependent polypeptide, where the modified
CC GLA domain comprises a glutamic acid residue at position 34. The
CC polypeptide is useful in modulating clot formation in mammals or in
CC treating certain types of haemophilia or clotting disorders. The membrane
CC binding affinity of polypeptides is increased by site directed
CC mutagenesis in the GLA domain. This sequence represents a vitamin K-
CC dependent protein of the invention.
XX
XX Sequence 44 AA;
SQ

Query Match      81.6%; Score 161.5; DB 7; Length 44;
Best Local Similarity 97.8%; Pred. No. 6.1e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLXRCXKXQCXSFXXARXIFKDXRTKLFWISY 45
   ||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1 ANA-FLXXLRPGSLXRCXKXQCXSFXXARXIFKDXRTKLFWISY 44

RESULT 4
ADQ26902
ID ADQ26902 standard; protein; 44 AA.
XX
XX ADQ26902;
AC
XX 26-AUG-2004 (first entry)
XX
XX Human factor VII gamma-carboxyglutamic acid (GLA) domain.
DE
XX Human; clot formation; protein C; activated protein C; APC;
XX gamma-carboxyglutamic acid domain; GLA domain; vitamin K-dependent;
KW
```

KW aspirin; warfarin; heparin; haemophilic disorder; haemostatic;
 KW anticoagulant; factor VII.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc-difference 1. .44
 FT /label= OTHER
 FT /note= "OTHER= All Xaa residues are glutamic acid or
 FT gamma carboxyglutamic acid"
 XX
 XX
 PN US6747003-B1.
 XX
 XX PD 08-JUN-2004.
 XX
 XX PF 03-FEB-2000; 2000US-00497591.
 XX
 XX PR 23-OCT-1997; 97US-00955636.
 XX PR 29-APR-1999; 99US-00302239.
 XX
 XX (MINU) UNIV MINNESOTA.
 XX PA
 XX Nelsestuen GL;
 XX
 XX DR WPI; 2004-429803/40.
 XX
 XX
 PT Decreasing clot formation by administering an anticoagulant agent, and a
 PT protein C or activated protein C polypeptide having a modified GLA
 PT domain, useful for treating hemophilic disorders in mammals.
 XX
 XX PS Example 5; SEQ ID NO 3; 4lpp; English.
 XX
 XX The invention relates to a method of decreasing clot formation comprising
 CC administering to a patient an anticoagulant agent and a protein C or
 CC activated protein C (APC) polypeptide comprising a modified gamma-
 CC carboxyglutamic acid (GLA) domain with two, three, four or five amino
 CC acid substitutions. The invention also relates to vitamin K-dependent
 CC nucleic acids, polypeptides, host cells, vectors and antibodies used in
 CC the methods of the invention. The anticoagulant agent is aspirin,
 CC warfarin or heparin, preferably aspirin. The methods and compositions of
 CC the present invention are useful for modulating clot formation for
 CC treating haemophilic disorders in mammals. This sequence represents the
 CC human factor VII GLA domain, used in the method of the invention.
 XX
 SQ Sequence 44 AA;
 Query Match 81.6%; Score 161.5; DB 8; Length 44;
 Best Local Similarity 97.8%; Pred. No. 6.1e-20; Mismatches 0; Indels 1; Gaps 1;
 Matches 44; Conservative 0;
 QY 1 ANAGFLXXLRPGSLRXKCKXXQCSPFXARXIFKDAKRTKLFWISY 45
 DB 1 ANA-FLXXLRPGSLRXKCKXXQCSPFXARXIFKDAKRTKLFWISY 44
 RESULT 5
 AAB84870
 ID AAB84870 standard; protein; 401 AA.
 XX
 AC AAB84870;
 XX
 XX 31-JUL-2001 (first entry)
 XX
 XX Mutant blood coagulant factor VII (FVII-31).
 XX
 KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 KW mutant; mutein.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 311. .317
 FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp -
 FT Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"

FT
 FT
 XX
 PN JP2001061479-A.
 XX
 PD 13-MAR-2001.
 XX
 XX PF 24-AUG-1999; 99JP-00237610.
 XX
 XX PR 24-AUG-1999; 99JP-00237610.
 XX
 XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX
 XX WPI; 2001-310677/33.
 DR N-PSDB; AAH19463.
 XX
 XX Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia.
 PT
 XX Claim 14; Page 20-21; 29pp; Japanese.
 XX
 XX The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-31. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients
 XX
 SQ Sequence 401 AA;
 Query Match 81.6%; Score 161.5; DB 4; Length 401;
 Best Local Similarity 75.6%; Pred. No. 5.9e-19; Mismatches 10; Indels 1; Gaps 1;
 Matches 34; Conservative 0;
 QY 1 ANAGFLXXLRPGSLRXKCKXXQCSPFXARXIFKDAKRTKLFWISY 45
 DB 1 ANA-FLXXLRPGSLRXKCKXXQCSPFXARXIFKDAKRTKLFWISY 44
 RESULT 6
 AAB84871
 ID AAB84871 standard; protein; 401 AA.
 XX
 AC AAB84871;
 XX
 XX 31-JUL-2001 (first entry)
 XX
 XX Mutant blood coagulant factor VII (FVII-39).
 XX
 KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 KW mutant; mutein.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 235. .239
 FT /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by Asp-
 FT Arg-Lys-Thr-Leu"
 FT Misc-difference 311. .317
 FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp -
 FT Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
 XX
 XX JP2001061479-A.
 XX
 XX 13-MAR-2001.
 XX
 XX PF 24-AUG-1999; 99JP-00237610.
 XX
 XX PR 24-AUG-1999; 99JP-00237610.
 XX
 XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX
 XX WPI; 2001-310677/33.
 DR N-PSDB; AAH19464.

ID	AAB84868	standard; protein; 406 AA.
XX		
XX		
FT	Misc-difference 235..239	/note= "wild-type Val-Pro-Gly-Thr substituted by Asp-
FT		

FT Arg-Lys-Thr-Leu"
 PN JP2001061479-A.
 XX 13-MAR-2001.
 PD
 XX 24-AUG-1999; 99JP-00237610.
 FF
 XX 24-AUG-1999; 99JP-00237610.
 PR
 XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 FA
 XX WPI; 2001-310677/33.
 DR N-PSDB; AAH19462.
 XX
 XX Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia.
 FT
 XX Claim 9; Page 17-18; 29pp; Japanese.
 PS
 XX The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-30. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients
 XX
 XX Sequence 406 AA;
 SQ
 Query Match 81.6%; Score 161.5; DB 4; Length 406;
 Best Local Similarity 75.6%; Pred. No. 6e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
 QY 1 ANAGFLXXLRPGSLRXCKXXQCSFXXARXIFKDXRXTKLFWISY 45
 DB 1 ANA-FLEELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 44
 FT
 RESULT 14
 ID AAB84866 standard; protein; 406 AA.
 XX
 AC AAB84866;
 XX
 XX 31-JUL-2001 (first entry)
 DT
 XX Wild-type human blood coagulant factor VII (FVII).
 DE
 XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia.
 KW
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Disulfide-bond 159..164
 FT
 XX JP2001061479-A.
 PN
 XX 13-MAR-2001.
 PD
 XX 24-AUG-1999; 99JP-00237610.
 PF
 XX 24-AUG-1999; 99JP-00237610.
 PR
 XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 PA
 XX WPI; 2001-310677/33.
 DR N-PSDB; AAH19459.
 XX
 XX Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia.
 FT
 XX Disclosure; Page 8-9; 29pp; Japanese.
 PS
 XX The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present

CC sequence represents the protein sequence for wild-type human FVII. The
 CC mutants can be used as an agent for the substitution therapy of
 CC haemophilia inhibitor patients
 XX
 SQ Sequence 406 AA;
 Query Match 81.6%; Score 161.5; DB 4; Length 406;
 Best Local Similarity 75.6%; Pred. No. 6e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
 QY 1 ANAGFLXXLRPGSLRXCKXXQCSFXXARXIFKDXRXTKLFWISY 45
 DB 1 ANA-FLEELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 44
 FT
 RESULT 15
 ID AAM52183 standard; protein; 406 AA.
 XX
 AC AAM52183;
 XX
 XX 07-FEB-2002 (first entry)
 DT
 XX Human FVII mutant V253N.
 DE
 XX
 KW Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
 KW cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
 KW myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
 KW muteln.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 6 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 7 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 14 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 16 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 19 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 20 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 25 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 26 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 29 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 35 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Modified-site 52 /note= "O-glycosylated"
 FT
 FT Modified-site 60 /note= "O-glycosylated"
 FT
 FT Modified-site 145 /note= "N-glycosylated"
 FT
 FT Cleavage-site 152..153
 FT /note= "proteolytic cleavage site converting FVII zymogen
 FT to an activated form, comprising two chains linked by a

FT		single disulphide bridge"
FT	Misc-difference 253	
FT	/note= "Wild-type Val substituted by Asn"	
FT	Modified-site 322	
FT	/note= "N-glycosylated"	
XX		
XX	WO200158935-A2.	
PN		
XX	16-AUG-2001.	
XX		
XX	12-FEB-2001; 2001WO-DK000094.	
PF		
XX	11-FEB-2000; 2000DK-00000218.	
PR	18-OCT-2000; 2000DK-00001558.	
XX		
XX	(MAXY-) MAXYGEN APS.	
PA		
XX		
PI	Andersen KV, Pedersen AH, Bornaes C;	
XX		
XX	WPI; 2001-581807/65.	
XX		
PT	New conjugate, useful for treating Factor VIIa related diseases or	
PT	disorders such as hemophilia, liver disease, myocardial infarction and	
PT	deep-vein thrombosis, comprises non-polypeptide group covalently attached	
PT	to polypeptide group.	
XX		
XX	Example 3; Page; 89pp; English.	
PS		
XX		
CC	The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)	
CC	polypeptide conjugates, comprising at least one non-polypeptide group	
CC	covalently attached to a polypeptide, where the amino acid sequence of	
CC	polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at	
CC	least one amino acid residue containing an attachment group for the non-	
CC	polypeptide group has been introduced or removed. The FVIIa conjugates	
CC	have haemostatic, thrombolytic, cardiac, hepatotrophic and	
CC	cerebroprotective activity and are useful for treating FVIIa/TF-related	
CC	diseases or disorders such as haemophilia, liver disease, myocardial	
CC	infarction, thrombotic stroke and deep-vein thrombosis. The conjugates	
CC	have increased functional in vivo half life and/or increased plasma half	
CC	life, increased bioavailability and or reduced sensitivity to proteolytic	
CC	degradation. Consequently medical treatment using the conjugates has a	
CC	number of advantages over currently available such as longer duration	
CC	from injections. The present sequence is that of a human FVII mutant,	
CC	having an addition in vivo glycosylation site and tested for its	
CC	amidolytic activity. Note: The present sequence is not shown in the	
CC	specification but is derived from the human wild-type FVII sequence shown	
CC	in SEQ ID NO 1 (AAM52171)	
XX		
XX	Sequence 406 AA;	
XX	XX	

```

Query Match      81.6%; Score 161.5; DB 4; Length 406;
Best Local Similarity 97.8; Pred. No. 6e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ANAGFLXXLRPGSLXRXCXQCXQCFXXARXIFKDXRTKLFWSY 45
    |||||
Db 1 ANA-FLAXLRPGSLXRXCXQCXQCFXXARXIFKDXRTKLFWSY 44
    |||||

```

Search completed: August 22, 2005, 18:45:41
Job time : 92 secs

```

Search completed: 1
Job time : 92 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2005, 09:28:04 ; Search time 25 Seconds
(without alignments)
173.190 Million cell updates/sec

Title: US10031005-3G4

Perfect score: 198

Sequence: 1 ANAGFLXXLRPGSLRXCKX.....XXARXIFKDAVTKLFWISY 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	161.5	81.6	466	1	KFHU7	coagulation factor
2	127.5	64.4	443	2	I46932	coagulation factor
3	119	60.1	407	1	KFB07	coagulation factor
4	98.5	49.7	461	1	JX0210	protein C (activat
5	95	48.0	617	2	S10511	thrombin (EC 3.4.2
6	95	48.0	618	2	AJ5827	thrombin (EC 3.4.2
7	93.5	47.2	456	1	KXBO	protein C (activat
8	93	47.0	416	1	KFBO	coagulation factor
9	91.5	46.2	488	1	EXHU	coagulation factor
10	91	46.0	461	1	KFHU	coagulation factor
11	90.5	45.7	492	1	EXBO	coagulation factor
12	89.5	45.2	461	1	S18994	protein C (activat
13	85.5	43.2	482	1	EXRT	coagulation factor
14	85	42.9	452	1	AJ0351	coagulation factor
15	85	42.9	459	2	J00419	coagulation factor
16	80.5	40.7	475	1	EXCH	coagulation factor
17	78	39.4	625	1	TBBO	thrombin (EC 3.4.2
18	73.5	37.1	461	1	KXHU	protein C (activat
19	73	36.9	622	1	TBHU	thrombin (EC 3.4.2
20	65	32.8	396	1	KXBOZ	plasma protein Z -
21	61.5	31.1	576	2	G96763	probable MAP kinase
22	60	30.3	422	1	KXHUZ	plasma protein Z p
23	58.5	29.5	642	2	S34333	plasma protein S p
24	57.5	29.0	594	2	D84859	probable MAP kinase
25	57.5	29.0	603	2	C96575	probable MAP kinase
26	56	28.3	675	1	KXBOS	plasma protein S p
27	55	27.8	673	2	A48089	growth arrest-spec
28	53.5	27.0	642	2	S34334	plasma protein S p
29	53.5	27.0	646	2	S38819	plasma protein S -

30	53.5	27.0	676	1	KXHUS	plasma protein S p
31	53	26.8	674	2	I55476	growth potentiatin
32	53	26.8	675	1	KXRTS	plasma protein S p
33	53	26.8	678	2	B48089	growth arrest-spec
34	52.5	26.5	675	1	KXMSS	plasma protein S p
35	46.5	23.5	516	2	H84424	probable MAP kinase
36	46	23.2	543	2	H84724	probable ARI-like
37	45.5	23.0	319	2	T15137	hypothetical prote
38	45	22.7	879	2	S55864	hypothetical prote
39	43.5	22.0	367	2	B56598	endothelial kinase
40	43.5	22.0	385	2	T15221	hypothetical prote
41	43.5	22.0	1298	2	A48999	protein-tyrosine k
42	43.5	22.0	1363	2	I58375	protein-tyrosine k
43	43.5	22.0	1379	2	JC4954	vascular endotheli
44	43	21.7	211	2	D96996	uncharacterized lo
45	43	21.7	402	2	C72226	hypothetical prote

ALIGNMENTS

coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human

C:Species: Homo sapiens (man)

C>Date: 19-May-1989 #sequence_revision 19-May-1994 #text_change 09-Jul-2004

C:Accession: A28322; A23819; A31186; B31186; S63524

R:O'Hara, P. J.; Grant, F. J.; Haldeman, B. A.; Gray, C. L.; Insley, M. Y.; Hagen, F. S.; Murri

Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987

A:Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depende

A:Reference number: A28322; MUID:87260948; PMID:3037537

A:Accession: A28322

A:Molecule type: DNA

A:Residues: 1-466 <OHA>

A:Cross-references: UNIPROT:P08709; GB:J02933; NID:9180333; PIDN:AAA51983.1; PID:9180334

R:Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C.

Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986

A:Title: Characterization of a cDNA coding for human factor VII.

A:Reference number: A23819; MUID:86205965; PMID:3486420

A:Accession: A23819

A:Molecule type: mRNA

A:Residues: 1-466 <HAG>

A:Cross-references: GB:M13232; NID:9182799; PIDN:AAA88040.1; PID:9182801

R:Thim, L.; Bjoern, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.F

Biochemistry 27, 7785-7793, 1988

A:Title: Amino acid sequence and posttranslational modifications of human factor VII-a f

A:Reference number: A90539; MUID:B9088153; PMID:3264725

A:Accession: A31186

A:Molecule type: protein

A:Residues: 61-212 <THI>

A:Accession: B31186

A:Molecule type: protein

A:Residues: 213-466 <PTH>

R:Bjoern, S.; Foster, D.C.; Thim, L.; Wiberg, F.C.; Christensen, M.; Komiyama, Y.; Peders

J. Biol. Chem. 266, 11051-11057, 1991

A:Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations at

A:Reference number: A40529; MUID:91250411; PMID:1904059

A:Contents: annotation; carbohydrate binding sites

R:Persson, E.; Petersen, L.C.

Eur. J. Biochem. 224, 293-300, 1995

A:Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carboxy

A:Reference number: S63524; MUID:96096752; PMID:8529655

A:Accession: S63524

A:Molecule type: protein

A:Residues: 61-65;99-103;105-109;213-217;308-312 <PER>

C:Genetics:

A:Gene: GDB:F7

A:Cross-references: GDB:I19897; OMIM:227500

A:Map position: 13q34-13q34

A:Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1

C:Function:

A:Description: catalyzes the proteolytic activation of coagulation factor X in the presen

coagulation factor IX in the presence of calcium and tissue factor

A;Pathway: blood coagulation extrinsic pathway
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-60/Domain: propeptide #status predicted <PRO>
F;21-60/Domain: Gla domain homology <GLA>
F;61-212/Product: coagulation factor VIIa light chain #status experimental <MA1>
F;110-141/Domain: EGF homology <EG1>
F;151-187/Domain: EGF homology <EG2>
F;213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F;213-447/Domain: trypsin homology <TRY>
F;66-67,74,76,79,80,85,86,89,95/Modified site: gamma-carboxyglutamic acid (Glu) #status
F;77-82,110-121,115-130,132-141,151-162,158-172,174-187,195-322,219-224,238-254,370-389,
F;112,120/Binding site: carboxylate (Ser) (covalent) #status experimental
F;123/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent
F;205,382/Binding site: carboxylate (Asn) (covalent) #status experimental
F;212-213/Cleavage site: Arg-11e (coagulation factor XIIa) #status experimental
F;253,302,404/Active site: His, Asp, Ser #status predicted
F;350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted

Query Match 81.6%; Score 161.5; DB 1; Length 466;
Best Local Similarity 75.6%; Pred. No. 3.1e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLRXKXQCSFXXARXIFPKDAXRTKLFWSY 45
Db 61 ANA-FLEELRPGSLRECKEQCSFEAREIFPKDAXRTKLFWSY 104

RESULT 2
146932
coagulation factor VII - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
C;Accession: I46932
R;Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
Thromb. Res. 69, 231-238, 1993
A;Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
A;Reference number: I46932; MUID:93190306; PMID:8383365
A;Accession: I46932
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-443 <BRO>
A;Cross-references: GB:S56300; NID:g266294; PID:g266295
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
F;24-83/Domain: Gla domain homology <GLA>
F;89-120/Domain: EGF homology <EG1>
F;130-166/Domain: EGF homology <EG2>
F;192-425/Domain: trypsin homology <TRY>

Query Match 64.4%; Score 127.5; DB 2; Length 443;
Best Local Similarity 57.8%; Pred. No. 1.6e-13;
Matches 26; Conservative 4; Mismatches 14; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLRXKXQCSFXXARXIFPKDAXRTKLFWSY 45
Db 40 ANS-FLEELRPGSLRECKEQCSFEAREVFQSTERTKQFWITY 83

RESULT 3
KF807
coagulation factor VIIa (EC 3.4.21.21) - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: A31979; C20274
R;Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.
J. Biol. Chem. 263, 14868-14877, 1988
A;Title: Bovine factor VII. Its purification and complete amino acid sequence.
A;Reference number: A31979; MUID:89008362; PMID:3049594
A;Accession: A31979
A;Molecule type: protein
A;Residues: 1-407 <TAK>
A;Cross-references: UNIPROT:P22457

R;McMullen, B.A.; Fujikawa, K.; Kiesel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor VIIa
A;Reference number: A20274; MUID:83308813; PMID:6688526
A;Accession: C20274
A;Molecule type: protein
A;Residues: 58-62, 'X', 64-68 <MCM>
A;Note: the residue designated 'X' was determined to be hydroxyaspartic acid
R;Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, S.
J. Biochem. 104, 867-868, 1988
A;Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factor IX
A;Reference number: A44556; MUID:89213999; PMID:3149637
A;Contents: annotation
A;Note: structure and location of covalently bound carbohydrate
C;Function:
A;Description: catalyzes the proteolytic activation of coagulation factor X in the presence of calcium and tissue factor
A;Pathway: blood coagulation extrinsic pathway
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
F;1-153/Product: coagulation factor VIIa light chain #status experimental <MA1>
F;1-44/Domain: Gla domain homology (fragment) <GLA>
F;50-81/Domain: EGF homology <EG1>
F;91-127/Domain: EGF homology <EG2>
F;153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F;153-387/Domain: trypsin homology <TRY>
F;6,7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #status
F;17-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-368/I
F;52/Binding site: carboxylate (Ser) (covalent) #status experimental
F;63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experimental
F;145,203/Binding site: carboxylate (Asn) (covalent) #status experimental
F;152-153/Cleavage site: Arg-11e (coagulation factor XIIa) #status experimental
F;193,242,344/Active site: His, Asp, Ser #status predicted
F;290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match 60.1%; Score 119; DB 1; Length 407;
Best Local Similarity 52.4%; Pred. No. 4.1e-12;
Matches 22; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 4 GFLXXLRPGSLRXKXQCSFXXARXIFPKDAXRTKLFWSY 45
Db 3 GFLLELPGSLRECKEQCSFEAREIFPKDAXRTKLFWSY 44

RESULT 4
JX0210
protein C (activated) (EC 3.4.21.69) precursor - mouse
N;Alternate names: vitamin K-dependent serine proteinase
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JX0210
R;Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
J. Biochem. 111, 491-495, 1992
A;Title: Isolation and characterization of a mouse protein C cDNA.
A;Reference number: JX0210; MUID:92316897; PMID:1618739
A;Accession: JX0210
A;Molecule type: mRNA
A;Residues: 1-461 <TAD>
A;Cross-references: UNIPROT:P33587; GB:D10445; NID:g220385; PIDN:BAA01235.1; PID:g220386
A;Experimental source: liver
C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that regulates blood coagulation

S.
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
F;1-33/Domain: signal sequence #status predicted <SIG>
F;127-85/Domain: Gla domain homology <GLA>
F;34-41/Domain: propeptide #status predicted <PRO>
F;42-196,199-461/Product: protein C #status predicted <PCR>
F;42-196/Domain: light chain #status predicted <PCL>
F;91-130/Domain: EGF homology <EG1>
F;139-174/Domain: EGF homology <EG2>
F;199-461/Domain: heavy chain #status predicted <PCH>
F;199-211/Domain: activation peptide #status predicted <ACT>

```

RESULT 6
A35827
thrombin (EC 3.4.21.5) precursor - mouse

```

A;Accession: A26250
A;Molecule type: mRNA
A;Residues: 1-456 <ION>
A;Cross-references: UNIPROT:P00745
R;Fernlund, P.; Stenflo, J.
J. Biol. Chem. 257, 12170-12179, 1982
A;Title: Amino acid sequence of the light chain of bovine protein C.
A;Reference number: A18385; MUID:83007325; PMID:6896876
A;Accession: A18385
A;Molecule type: protein
A;Residues: 40-194 <FER>
A;Note: 82-Lys was also found
R;Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.
Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983
A;Title: Beta-Hydroxyaspartic acid in vitamin K-dependent protein C.
A;Reference number: A19316; MUID:83169769; PMID:6572939
A;Contents: annotation; revision to residue 110

A;Accession: A42485
A;Molecule type: DNA
A;Residues: 1-15 <MIA>
A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIN:93780, NCBI:93787)
R;Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.
Gene 41, 311-314, 1986
A;Title: Isolation and characterization of human blood-coagulation factor X cDNA.
A;Reference number: A25853; MUID:86221713; PMID:3011603
A;Accession: A25853
A;Molecule type: mRNA
A;Residues: 19-284, 'B', 289-488 <KAU>
A;Cross-references: GB:W22613; NID:g180335; PIDN:AAAS1984.1; PID:g180336
R;Fung, M.R.; Hay, C.W.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985
A;Title: Characterization of an almost full-length cDNA coding for human blood coagulation factor X.
A;Reference number: A22208; MUID:85216545; PMID:2582420
A;Accession: A22208
A;Molecule type: mRNA
A;Residues: 13-441, 'S', 443-488 <FNU>
A;Cross-references: GB:K03194; NID:g182840; PIDN:AAAS2490.1; PID:g182841
R;Levtus, S.P.; Chung, D.W.; Kiesel, W.; Kurachi, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 81, 3695-3702, 1984
A;Title: Characterization of a cDNA coding for human factor X.
A;Reference number: A21284; MUID:8422026; PMID:6587384
A;Accession: A21284
A;Molecule type: mRNA
A;Residues: 13-284, 'B', 289-488 <L82>
A;Cross-references: GB:K01886
R;McMullen, B.A.; Fujikawa, K.; Kiesel, W.; Saagawa, T.; Howald, W.N.; Kwa, E.Y.; Weinsbach, R.S.
Biochemistry 22, 2875-2884, 1983
A;Title: Complete amino acid sequence of the light chain of human blood coagulation factor X.
A;Reference number: A20362; MUID:83257207; PMID:6871167
A;Accession: A20362
A;Molecule type: protein
A;Residues: 41-179 <MCM>
R;Inoue, K.; Morita, T.
Eur. J. Biochem. 218, 153-163, 1993
A;Title: Identification of O-linked oligosaccharide chains in the activation peptides of human blood coagulation factor X.
A;Reference number: S39414; MUID:94062825; PMID:8243461
A;Accession: S39415
A;Molecule type: protein
A;Residues: 183-234 <INO>
A;Note: glycosylation sites
A;Note: identification and characterization of beta-hydroxyaspartic acid
R;Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhusan, K.; Lyman, G.
Gene 84, 517-519, 1989
A;Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human blood coagulation factor X.
A;Reference number: I54051; MUID:90128299; PMID:2612918
A;Accession: I54051
A;Status: translation not shown; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-23 <RES>
A;Cross-references: GB:M33297; NID:g183860; PIDN:AAAS2636.1; PID:G553330
R;Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Blass, R.J.
Mol. Biol. 232, 947-966, 1993
A;Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
A;Reference number: A49458; MUID:93360277; PMID:8355279
A;Contents: annotation; X-ray crystallography, 2.2 angstroms
C;Comment: The two chains held together by one disulfide bond are formed from a single-coding sequence.
C;Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) of the blood coagulation cascade.
C;Genetics:
A;Gene: GDB:F10
A;Cross-references: GDB:113890; OMIM:227600
A;Map position: 13q34-13q34
A;Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
A;Note: deficiency of this factor causes Stuart disease
C;Function:
A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of factor V and calcium ions.
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate; disulfide bond; protein structure
F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-40/Domain: propeptide #status predicted <PRO>
F;25-84/Domain: Gla domain homology <GLA>
F;41-179/Product: coagulation factor X light chain #status experimental <LCH>
F;90-121/Domain: EGF homology <EG1>
F;129-164/Domain: EGF homology <EG2>
F;183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
F;183-234/Domain: activation peptide #status experimental <APT>
F;235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
F;235-462/Domain: trypsin homology <TRY>
F;46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F;57-62/Diulfide bonds: #status Predicted
F;90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/I
F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F;199,211/Binding site: carbohydrtate (Thr) (covalent) #status experimental
F;221,231/Binding site: carbohydrtate (Asn) (covalent) #status experimental
F;234-235/Cleavage site: Arg-Ile (Coagulation factor IXa, coagulation factor VIIa) #stat
F;276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 46.2%; Score 91.5; DB 1; Length 488;
Best Local Similarity 40.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 8; Mismatches 18; Indels 1; Gaps 1;

Qy 1 ANAGFLXLRPGSLRXKXKXQCSFXXARXIFKDAXRKLFWISY 45
41 ANS-FLEEMKGLHRCMBETCSYEAREVFEDSDKTNFNNKY 84
Db

RESULT 10
KPHU
coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human
N;Alternate names: antihemophilic factor B; Christmas factor
C;Species: Homo sapiens (man)
C;Date: 17-Dec-1982 #sequence revision 30-Jun-1987 #text change 09-Jul-2004
C;Accession: A00922; A37570; A30511; A32989; A22673; A21337; A37546; A30623; A60486; A20:
R;Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.
Biochemistry 24, 3736-3750, 1985
A;Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).
A;Reference number: A00922; MUID:86000558; PMID:2994716
A;Accession: A00922
A;Molecule type: DNA
A;Residues: 1-461 <YOS>
A;Cross-references: UNIPROT:P00740; GB:K02402; NID:g182612; PIDN:AAB59620.1; PID:g182613
R;Anson, D.S.; Choo, K.H.; Rees, D.J.G.; Giannelli, F.; Gould, K.; Huddleston, J.A.; Brov
EMBO J. 3, 1053-1060, 1984
A;Title: The gene structure of human anti-haemophilic factor IX.
A;Reference number: A37570; MUID:842336100; PMID:6329734
A;Accession: A37570
A;Molecule type: DNA
A;Residues: 1-461 <RES>
A;Cross-references: GB:K02048
R;Reitsma, P.H.; Bertina, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Briet, E.
Blood 72, 1074-1076, 1988
A;Title: The putative factor IX gene promoter in hemophilia B Leyden.
A;Reference number: A30511; MUID:88327116; PMID:3416069
A;Accession: A30511
A;Molecule type: DNA
A;Residues: 8-24 <RET>
A;Cross-references: EMBL:X55008; NID:g311288; PIDN:CAB38245.2; PID:g4469253
R;Roebert, D.D.; Bottema, C.D.K.; Buerstedde, J.M.; Sommer, S.S.
Am. J. Hum. Genet. 45, 448-457, 1989
A;Title: Functionally important regions of the factor IX gene have a low rate of polymor
A;Reference number: A32989; MUID:89371752; PMID:2773937
A;Accession: A32989
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 30-92 <ROE>
R;McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; St
Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985
A;Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulati
A;Reference number: A22673; MUID:85190593; PMID:3857619
A;Accession: A22673
A;Molecule type: mRNA
A;Residues: 1-193, 'T', 195-461 <MCG>

A;Cross-references: GB:M11309; NID:g180552; PIDN:AAA52023.1; PID:g180553
 A;Note: the authors translated the codon ACA for residue 29 as TYR
 R;Jaye, M.; de la Salle, H.; Schamber, F.; Balland, A.; Kohli, V.; Findel, A.; Tolstosh
 Nucleic Acids Res. 11, 2325-2335, 1983
 A;Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-ba
 A;Reference number: A21337; MUID:83220788; PMID:6687940
 A;Accession: A21337
 A;Molecule type: mRNA
 A;Residues: 1-193, 'T', 195-461 <JAY>
 A;Cross-references: GB:J00137; NID:g182610; PIDN:AAA52763.1; PID:g182611
 R;Jagadeeswaran, P.; Laville, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.
 Somat. Cell Mol. Genet. 10, 465-473, 1984
 A;Title: Isolation and characterization of human factor IX cDNA: identification of Tag I
 A;Reference number: A37546; MUID:84300526; PMID:6089357
 A;Accession: A37546
 A;Molecule type: mRNA
 A;Residues: 38-193, 'T', 195-326 <JAG>
 A;Cross-references: GB:M35672
 R;Kurachi, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982
 A;Title: Isolation and characterization of a cDNA coding for human factor IX.
 A;Reference number: A30623; MUID:83065193; PMID:6959130
 A;Accession: A30623
 A;Molecule type: mRNA
 A;Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A',
 A;Cross-references: GB:J00136; NID:g182608; PIDN:AAA98726.1; PID:g182609
 A;Experimental source: liver
 R;Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.
 Vox Sang. 58, 21-29, 1990
 A;Title: Development of an immunoaffinity process for factor IX purification.
 A;Reference number: A60486; MUID:90194857; PMID:2316207
 A;Accession: A60486
 A;Molecule type: protein
 A;Residues: 47-52, 'XX', 55-60, 'X', 62, 'XX', 65 <THA>
 R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
 A;Reference number: A20274; MUID:83308813; PMID:6688526
 A;Accession: A20274
 A;Molecule type: protein
 A;Residues: 105-109, 'X', 111-115 <MCW>
 R;Balland, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Sall
 Eur. J. Biochem. 172, 565-572, 1988
 A;Title: Characterisation of two differently processed forms of human recombinant factor
 A;Reference number: S02527; MUID:88166735; PMID:3280312
 A;Accession: S02527
 A;Molecule type: protein
 A;Residues: 29-63 <BAL>
 A;Note: processed forms expressed in recombinant system
 R;Jallat, S.; Perraud, F.; Dalemans, W.; Balland, A.; Dieterle, A.; Faure, T.; Meulien,
 EMBO J. 9, 3295-3301, 1990
 A;Title: Characterization of recombinant human Factor IX expressed in transgenic mice an
 A;Reference number: S12058; MUID:91006024; PMID:2209546
 A;Accession: S12058
 A;Molecule type: mRNA; protein
 A;Residues: 1-68 <JAL>
 A;Note: processed forms expressed in recombinant system
 R;Handford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campbe
 EMBO J. 9, 475-480, 1990
 A;Title: The first EGF-like domain from human factor IX contains a high-affinity calcium
 A;Reference number: S12377; MUID:90151623; PMID:2406129
 A;Accession: S12377
 A;Molecule type: protein
 A;Residues: 92-130 <HAN>
 A;Note: NMR detection of calcium binding by domain expressed in recombinant system
 R;de la Salle, C.; Charmanlier, J.L.; Baas, M.J.; Schwartz, A.; Wiesel, M.L.; Grunebaum,
 Thromb. Haemost. 70, 370-371, 1993
 A;Title: A deletion located in the 3' non translated part of the factor IX gene responsi
 A;Reference number: I59612; MUID:94054330; PMID:8236150
 A;Accession: I59612
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 444-461 <RES>

A;Cross-references: GB:S66752; NID:g439773; PIDN:AAB28588.1; PID:g439774
 R;Stoflet, E.S.; Koebel, D.D.; Sarkar, G.; Sommer, S.S.
 Science 239, 491-494, 1988
 A;Title: Genomic amplification with transcript sequencing.
 A;Reference number: I59529; MUID:88127096; PMID:3340835
 A;Accession: I59529
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 230-359 <RE2>
 A;Cross-references: GB:M19063; NID:g182622; PIDN:AAA52456.1; PID:g182623
 R;Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimonishi, Y.; Nishimura, H.; Iw
 Biochemistry 33, 5167-5171, 1994
 A;Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically link
 A;Reference number: A54255; MUID:94227047; PMID:8172892
 A;Accession: A54255
 A;Molecule type: protein
 A;Residues: 'D', 204, 'X', 206-211, 212, 'D', 214, 'X', 216-221, 'D' <AGA>
 A;Note: the residues designated 'X' were determined to be threonine bound to carbohydrate
 R;Di Scipio, R.G.; Kurachi, K.; Davie, E.W.
 J. Clin. Invest. 61, 1528-1538, 1978
 A;Title: Activation of human factor IX (Christmas factor).
 A;Reference number: A18483; MUID:78194509; PMID:659613
 A;Contents: annotation; activation; active site; carbohydrate binding
 R;McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.
 Am. Soc. Hematol. Abstr. 64 (Suppl.1), 262a, 1984
 A;Reference number: A37569
 A;Contents: annotation
 A;Note: 194-Thr was also found
 R;Morita, T.; Isaacs, B.S.; Emon, C.T.; Johnson, A.E.
 J. Biol. Chem. 259, 5698-5704, 1984
 A;Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding
 A;Reference number: A37543; MUID:84185715; PMID:6425296
 A;Contents: annotation; calcium binding
 R;Morita, T.; Isaacs, B.S.; Emon, C.T.; Johnson, A.E.
 J. Biol. Chem. 260, 2583, 1985
 A;Reference number: A37544
 A;Contents: annotation; calcium binding, correction
 R;Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.
 Cell 45, 343-348, 1986
 A;Title: Defective propeptide processing of blood clotting factor IX caused by mutation c
 A;Reference number: A37545; MUID:86189947; PMID:3009023
 A;Contents: annotation; signal sequence cleavage site
 R;Suehiro, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya,
 J. Biol. Chem. 264, 21257-21265, 1989
 A;Title: Blood clotting factor IX B(M) Nagoya: substitution of arginine 180 by tryptophan
 A;Reference number: A30622; MUID:90078229; PMID:2592373
 A;Contents: annotation; sequence of mutant B(M) Nagoya
 A;Note: carboxylation, glycosylation, and cleavage sites
 R;Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, P.A.; Mayhew, M.; Tse, A.G.D.; Brownlee
 submitted to the Brookhaven Protein Data Bank, November 1991
 A;Reference number: A51252; PDB:1IXA
 A;Contents: annotation; conformation by (1)H-NMR, residues 92-130
 A;Note: recombinant form expressed in yeast
 C;Comment: Factor IX is activated by factor XIa, which excises the activation peptide pro
 C;Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K-
 C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stron
 C;Genetics:
 A;Gene: GDB:F9
 A;Cross-references: GDB:119900; OMIM:306900
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 A;Introns: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1
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 A;Description: catalyzes the proteolytic activation of coagulation factor X in the preser
 A;Pathway: blood coagulation intrinsic pathway
 C;Keywords: coagulation factor X; EGF homology; Gla domain homology; trypsin homology.
 C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutami
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 F;29-46/Domain: propeptide #status experimental <PPT>
 F;31-91/Domain: Gla domain homology <GLA>
 F;47-131/Product: coagulation factor IXa light chain #status experimental <ALC>
 F;97-128/Domain: EGF homology <EG1>
 F;134-170/Domain: EGF homology <EG2>
 F;192-226/Domain: activation peptide #status experimental <ACT>

A;Title: Bovine factor X-la (activated Stuart factor). Evidence of homology with mammali
A;Reference number: A12453; MUID:73053314; PMID:4264286
A;Contents: annotation; active site
R;Fujikawa, K.; Titani, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
A;Title: Activation of bovine factor X (Stuart factor): conversion of factor Xaalpha to f
A;Reference number: A13504; MUID:76053121; PMID:1059122
A;Contents: annotation; activation
R;Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.
J. Biol. Chem. 259, 5705-5710, 1984
A;Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic
A;Reference number: A38024; MUID:84185716; PMID:6546930
A;Contents: annotation; calcium binding
R;Morita, T.; Jackson, C.M.
J. Biol. Chem. 261, 4008-4014, 1986
A;Reference number: A38025; MUID:86140210; PMID:3949800
A;Contents: annotation; sulfate binding
C;Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
C;Comment: The two chains are formed from a single-chain precursor by the excision of tw
C;Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), o
activation.

C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro
C;Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin
C;Genetics:
A;Gene: F10
A;Map position: 13q34
C;Function:

A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
A;Pathway: blood coagulation
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-40/Domain: propeptide #status predicted <PRO>
F;25-84/Domain: Gla domain homology <GLA>
F;41-180/Product: coagulation factor X light chain #status experimental <LCH>
F;90-121/Domain: EGF homology <EGE>
F;129-164/Domain: EGF homology <EG2>
F;183-492/Product: coagulation factor X heavy chain #status experimental <HCH>
F;183-233/Domain: activation peptide #status experimental <APT>
F;234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>
F;234-461/Domain: trypsin homology <TRY>

F;46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #st
F;57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-341/Disulfide bonds: #status pi
F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F;200/Binding site: sulfite (Tyr) (covalent) (partial) #status experimental
F;208,485/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;233-234/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #statu
F;240-245,260-276,389-403,414-442/Disulfide bonds: #status experimental
F;275,321,418/Active site: His, Asp, Ser #status predicted

Query Match 45.7%; Score 90.5; DB 1; Length 492;
Best Local Similarity 42.2%; Pred. No. 3.le-07;
Matches 19; Conservative 7; Mismatches 18; Indels 1; Gaps 1;

QY 1 ANAGFLXLRPGSLRXCKXCQCFFXXARXIFKDXRTKLFWISY 45
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DB 41 ANS-FLEEVKGNLRECLEACSLSEAREVPDEAQTDPEWSKY 84
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RESULT 12
S18994
protein C (activated) (EC 3.4.21.69) precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S18994; S24312
R;Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
submitted to the EMBL Data Library, February 1992
A;Description: The cDNA cloning and mRNA expression of rat protein C.
A;Reference number: S18994
A;Accession: S18994
A;Status: preliminary
A;Molecule type: mRNA

Search completed: August 22, 2005, 18:46:44
Job time : 26 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2005, 09:28:04 ; Search time 83 Seconds
(without alignment)
277.633 Million cell updates/sec

Title: US10031005-3G4

Perfect score: 198

Sequence: 1 ANAGFLXLRGSLRXCKX.....XXARXIFKDXRTKLFWISY 45

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	DB	ID	Description
1	161.5	81.6	466	1 FA7_HUMAN	P08709 homo sapien
2	161.5	81.6	679	2 Q96PQ8	Q96PQ8 homo sapien
3	127.5	64.4	444	1 FA7_RABIT	P98139 oryctolagus
4	119	60.1	407	1 FA7_BOVIN	P22457 bos taurus
5	118	59.6	443	2 Q8JHC9	Q8JHC9 brachydanio
6	116.5	58.8	446	1 FA7_MOUSE	P70375 mus musculus
7	103.5	52.3	459	1 PRTC_PIG	Q961p2 mus scrofa
8	103	52.0	442	2 Q804X1	Q804x1 fugu rubrip
9	101	51.0	537	2 Q804W8	Q804w8 fugu rubrip
10	98.5	49.7	460	1 PRTC_MOUSE	P33587 mus musculus
11	95	48.0	218	1 TWG1_HUMAN	O14668 homo sapien
12	95	48.0	266	2 Q8NEK6	Q8NEK6 homo sapien
13	95	48.0	617	1 THRB_RAT	P18292 rattus norv
14	95	48.0	618	1 THRB_MOUSE	P19221 mus musculus
15	93.5	47.2	446	1 FA7_RAT	Q8K3u6 rattus norv
16	93.5	47.2	456	1 PRTC_BOVIN	P00745 bos taurus
17	93	47.0	49	2 Q95ME8	Q95ME8 bos taurus
18	93	47.0	416	1 FA9_BOVIN	P00741 bos taurus
19	92.5	46.7	462	2 Q6PAG2	Q6pag2 xenopus lae
20	92	46.5	179	2 Q8TAS3	Q8tas3 homo sapien
21	92	46.5	198	1 TWG2_MOUSE	Q8182 mus musculus
22	92	46.5	202	1 TWG2_HUMAN	O14669 homo sapien
23	91.5	46.2	488	1 FA10_HUMAN	P00742 homo sapien
24	91	46.0	433	2 Q8JHD0	Q8jhd0 brachydanio
25	91	46.0	433	2 Q90YK1	Q90yk1 brachydanio
26	91	46.0	461	1 FA9_HUMAN	P00740 homo sapien
27	91	46.0	461	1 FA9_PANTR	Q95nd7 pan troglod
28	91	46.0	461	2 Q95ND6	Q95nd6 pan troglod
29	90.5	45.7	425	2 Q804X7	Q804x7 gallus gall
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RESULT 1
FA7_HUMAN
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AC P08709; Q14339;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator) (SPCA) (Proconvartin) (Eptacog alfa).
GN Name=F7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86205965; PubMed=3486420;
RA Hagen F.S., Gray C.H., O'Hara P.J., Grant F.J., Grant F.J., Saari G.C.,
RA Woodbury R.G., Hart C.E., Inley M.Y., Kiesel W., Kurachi K.,
RA Davie E.W.;
RT "Characterization of a cDNA coding for human factor VII.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260948; PubMed=3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Inley M.Y.,
RA Hagen F.S., Murray M.J.;
RT "Nucleotide sequence of the gene coding for human factor VII, a
RT vitamin K-dependent protein participating in blood coagulation.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.
RA Rieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi O., Nickerson D.A.;
RT "SeattleSNPs: NHLBI HL66682 program for genomic applications, UW-
RT FHCR, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=89088153; PubMed=3264725;
RA Thim L., Bjoern S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,
RA Pedersen A.H., Hedner U.;
RT "Amino acid sequence and posttranslational modifications of human
RT factor VIIa from plasma and transfected baby hamster kidney cells.";
RL Biochemistry 27:7785-7793(1988).
RN [5]
RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RX MEDLINE=91250411; PubMed=1904059;
RA Bjoern S., Foster D.C., Thim L., Wiberg F.C., Christensen M.,
RA Komiya Y., Pedersen A.H., Kiesel W.;
RT "Human plasma and recombinant factor VII. Characterization of O-
RT glycosylations at serine residues 52 and 60 and effects of site-
RT directed mutagenesis of serine 52 to alanine.";

32 89.5 45.2 461 1 PRTC_RAT
33 89.5 45.2 461 2 Q88FY8
34 89 44.9 216 2 Q6DIH4
35 88.5 44.7 433 2 Q804X5
36 88 44.4 466 2 Q6SA95
37 87.5 44.2 490 1 FA10_RABIT
38 86 43.4 208 2 Q6GPI7
39 86 43.4 376 1 FA10_TROCA
40 85.5 43.2 469 2 Q9GMD9
41 85.5 43.2 482 1 FA10_RAT
42 85 42.9 434 2 Q7T3B6
43 85 42.9 452 1 FA9_CANFA
44 85 42.9 459 1 FA9_MOUSE
45 84 42.4 376 1 FA10_HOPST

ALIGNMENTS

RL J. Biol. Chem. 266:11051-11057(1991).
RN [6]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=90062160; PubMed=2511201;
RA Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T., Takao T.,
RA Shimonishi Y., Iwanaga S.;
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
RT epidermal growth factor-like domain of human factors VII and IX and
RT protein Z and bovine protein Z.";
RL J. Biol. Chem. 264:20320-20325(1989).
RN [7]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z.";
RL Adv. Exp. Med. Biol. 281:121-131(1990).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=96175641; PubMed=8598903; DOI=10.1038/380041a0;
RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
RT "The crystal structure of the complex of blood coagulation factor VIIa
RT with soluble tissue factor.";
RL Nature 380:41-46(1996).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=99126538; PubMed=9925787; DOI=10.1006/jmbi.1998.2452;
RA Zhang E., St. Charles R., Tulinsky A.;
RT "Structure of extracellular tissue factor complexed with factor VIIa
RT inhibited with a BPRI mutant.";
RL J. Mol. Biol. 285:2089-2104(1999).
RN [10]
RP STRUCTURE BY NMR OF 105-145.
RX MEDLINE=98367502; PubMed=9692950; DOI=10.1021/bi980522f;
RA Muranyi A., Finn B.S., Gippert G.P., Forsen S., Stenflo J.,
RA Drakenberg T.;
RT "Solution structure of the N-terminal EGF-like domain from human
RT factor VII.";
RL Biochemistry 37:10605-10615(1998).
RN [11]
RP VARIANT GLN-364.
RX MEDLINE=91300046; PubMed=2070047;
RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
RA Meade T.W., Tuddenham E.G.D.;
RT "Purification and characterization of factor VII 304-Gln: a variant
RT molecule with reduced activity isolated from a clinically unaffected
RT male.";
RL Blood 78:132-140(1991).
RN [12]
RP VARIANTS GLN-364 AND PHE-370.
RX MEDLINE=92340074; PubMed=1634227;
RA Marchetti G., Patraccchini P., Gemmati D., Derosa V., Pinotti M.,
RA Rodorigo G., Caonato A., Girolami A., Bernardi F.;
RT "Detection of two missense mutations and characterization of a repeat
RT polymorphism in the factor VII gene (F7).";
RL Hum. Genet. 89:497-502(1992).
RN [13]
RP VARIANT TYR-238.
RX MEDLINE=93372811; PubMed=8364544;
RA Marchetti G., Ferrati M., Patraccchini P., Redaelli R., Bernardi F.;
RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms
RT (115His and 333Ser) in the human coagulation factor VII gene.";
RL Hum. Mol. Genet. 2:1055-1056(1993).
RN [14]
RP VARIANTS.
RX MEDLINE=94061028; PubMed=8242057;
RA Takamiya O., Kembali-Cook G., Martin D.M.A., Cooper D.N.,
RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,
RA Tuddenham E.G.D., McVey J.H.;
RT "Detection of missense mutations by single-strand conformational
RT polymorphism (SSCP) analysis in five dysfunctional variants of

RT coagulation factor VII.";
RL Hum. Mol. Genet. 2:1355-1359(1993).
RN [15]
RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.
RX MEDLINE=94264305; PubMed=8204879;
RA Chaing S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
RT "Severe factor VII deficiency caused by mutations abolishing the
RT cleavage site for activation and altering binding to tissue factor.";
RL Blood 83:3524-3535(1994).
RN [16]
RP VARIANT SER-367.
RX PubMed=7860081;
RA Dewald G., Noethen M.M., Ruther K.;
RT "A common Ser/Thr polymorphism in the perforin-homologous region of
RT human complement component C7.";
RL Hum. Hered. 44:301-304(1994).
RN [17]
RP VARIANT VAL-354.
RX MEDLINE=95072589; PubMed=7981691;
RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
RA Rodeghiero F., Marchetti G.;
RT "Topologically equivalent mutations causing dysfunctional coagulation
RT factors VII (294Ala-->Sval) and X (334Ser-->Pro).";
RL Hum. Mol. Genet. 3:1175-1177(1994).
RN [18]
RP VARIANT MIE HIS-307.
RX MEDLINE=95064662; PubMed=7974346;
RA Ohiwa M., Hayaashi T., Wada H., Minamikawa K., Shirakawa S., Suzuki K.;
RT "Factor VII M1e: homozygous asymptomatic type I deficiency caused by
RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
RT catalytic domain.";
RL Thromb. Haemost. 71:773-777(1994).
RN [19]
RP VARIANT MET-419.
RX MEDLINE=96247510; PubMed=8652821;
RA Arbini A.A., Mannucci P.M., Bauer K.A.;
RT "A Thr359Met mutation in factor VII of a patient with a hereditary
RT deficiency causes defective secretion of the molecule.";
RL Blood 87:5085-5094(1996).
RN [20]
RP VARIANTS TRP-283; LYS-325; VAL-358; GLN-364; GLU-402 AND GLN-413.
RX MEDLINE=97001216; PubMed=8844208;
RA DOI=10.1002/(SICI)1098-1004(1996)8:2<108::AID-HUMU2>3.3.CO;2-6;
RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
RA Lunghi B., Rodeghiero F., Marchetti G.;
RT "Mutation pattern in clinically asymptomatic coagulation factor VII
RT deficiency.";
RL Hum. Mutat. 8:108-115(1996).
RN [21]
RP VARIANT VAL-304.
RX MEDLINE=97037613; PubMed=8883260;
RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M., Zaizov R.,
RA Seligsohn U.;
RT "Ala244Val is a common, probably ancient mutation causing factor VII
RT deficiency in Moroccan and Iranian Jews.";
RL Thromb. Haemost. 76:283-291(1996).
RN [22]
RP VARIANT MORIOKA PRO-13.
RX MEDLINE=98235713; PubMed=9576180;
RA Ozawa T., Takikawa Y., Niya K., Ejiri N., Suzuki K., Sato S.,
RA Sakuragawa N.;
RT "Factor VII Moriooka (FVII L-26P): a homozygous missense mutation in
RT the signal sequence identified in a patient with factor VII
RT deficiency.";
RL Br. J. Haematol. 101:47-49(1998).
RN [23]
RP VARIANTS MALTA THR-194 AND VAL-304.
RX MEDLINE=98112461; PubMed=9452082;
RA Alehinawi C., Scerri C., Galdies R., Aquilina A., Felice A.E.;
RT "Two new missense mutations (P134T and A244V) in the coagulation
RT factor VII gene.";

25-OCT-2004 (Rel. 45, Last annotation update)
 Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
 Name=F7; Synonyms=Cf7;
 Mus musculus (Mouse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 TISSUE=Liver;
 RX MEDLINE=96276538; PubMed=8701412;
 RA Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
 "Nucleotide structure and characterization of the murine blood coagulation factor VII gene.";
 RT Thromb. Haemost. 76:957-964(1996).
 [2]
 SEQUENCE FROM N.A.
 RX MEDLINE=97127167; PubMed=8972017;
 RA Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
 "Nucleotide structure and characterization of the murine blood coagulation factor VII gene.";
 RT Thromb. Haemost. 76:957-964(1996).
 CC -1- FUNCTION: Initiates the extrinsic pathway of blood coagulation. Serine protease that circulates in the blood in a zymogen form. Factor VII is converted to factor VIIa by factor Xa, factor XIIa, factor IXa, or thrombin by minor proteolysis. In the presence of tissue factor and calcium ions, factor VIIa then converts factor X to factor IXa by limited proteolysis. Factor VIIa will also convert to factor IX to factor IXa in the presence of tissue factor and calcium (By similarity).
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-Ile bond in factor X to form factor Xa.
 CC -1- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by a disulfide bond (By similarity).
 CC -1- TISSUE SPECIFICITY: Plasma.
 CC -1- PTM: The vitamin K-dependent, enzymatic carboxylation of some glutamate residues allows the modified protein to bind calcium (By similarity).
 CC -1- SIMILARITY: Belongs to the peptidase S1 family.
 CC -1- SIMILARITY: Contains 2 EGF-like domains.
 CC -1- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla) domain.

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 EMBL; U4795; AAC52570.1; -;
 DR EMBL; U66079; AAC33796.1; -;
 DR HSP; P08709; 1BF9.
 DR MEROPS; S01.215; -;
 DR MGD; MGI.109325; F7.
 DR InterPro; IPR000152; Aex_hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_II.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002383; Gla_blood.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR009003; Pept_ser_Cys.
 DR InterPro; IPR000294; VitK_dep_Gla.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; EGFBL0010; EGFBL0010.
 DR PRINTS; PR00001; GLABLOOD.

DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS00998; GLA_2; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Calcium-binding; EGF-like domain;
 KW Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;
 KW Plasma; Repeat; Serine protease; Signal; Vitamin K; Zymogen.
 FT SIGNAL 1 24 Potential.
 FT PROPEP 25 41 Potential.
 FT CHAIN 42 193 Factor VII light chain.
 FT CHAIN 194 446 Factor VII heavy chain.
 FT DOMAIN 42 86 Gla.
 FT DOMAIN 87 123 EGF-like 1, calcium-binding (Potential).
 FT DOMAIN 128 169 EGF-like 2.
 FT DOMAIN 194 446 Serine protease.
 FT SITE 193 194 Substrate (By similarity).
 FT ACT_SITE 234 234 By similarity.
 FT ACT_SITE 283 283 By similarity.
 FT ACT_SITE 385 385 By similarity.
 FT BINDING 379 379 Substrate (By similarity).
 FT DISULFID 58 63 By similarity.
 FT DISULFID 91 102 By similarity.
 FT DISULFID 96 111 By similarity.
 FT DISULFID 113 122 By similarity.
 FT DISULFID 132 143 By similarity.
 FT DISULFID 139 153 By similarity.
 FT DISULFID 155 168 By similarity.
 FT DISULFID 176 303 By similarity.
 FT DISULFID 200 205 By similarity.
 FT DISULFID 219 235 By similarity.
 FT DISULFID 351 370 By similarity.
 FT DISULFID 381 409 By similarity.
 FT MOD_RES 47 47 4-carboxyglutamate.
 FT MOD_RES 48 48 4-carboxyglutamate.
 FT MOD_RES 55 55 4-carboxyglutamate.
 FT MOD_RES 57 57 4-carboxyglutamate.
 FT MOD_RES 60 60 4-carboxyglutamate.
 FT MOD_RES 61 61 4-carboxyglutamate.
 FT MOD_RES 66 66 4-carboxyglutamate.
 FT MOD_RES 67 67 4-carboxyglutamate.
 FT MOD_RES 70 70 4-carboxyglutamate.
 FT MOD_RES 76 76 4-carboxyglutamate.
 FT MOD_RES 104 104 3-hydroxyaspartate (By similarity).
 FT CARBOHYD 186 186 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 244 244 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 99 99 G -> V (in Ref. 2).
 SQ SEQUENCE 446 AA; 50276 MW; 2512E44A45CBC96E CRC64;
 Query Match 58.8%; Score 116.5; DB 1; Length 446;
 Best Local Similarity 57.8%; Pred. NO. 1.9e-11;
 Matches 26; Conservative 1; Mismatches 17; Indels 1; Gaps 1;
 QY 1 ANAGFLXLRPGSLRXKXQCSFYXARXIFKDXRTKLFWSY 45
 DB 42 ANS-LLEELWPGSLERECEEQCSFEAREIFKSPERTKQFWIV 85
 RESULT 7
 ID_PRTC_PIG STANDARD; PRT; 459 AA.
 AC O9GLE2; AC
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Vitamin K-dependent protein C precursor (EC 3.4.21.69)
 DE (Anticoagthrombin IIA) (Anticoagulation protein C) (Blood coagulation
 factor XIV)
 GN Name=PROC;
 OS Sus scrofa (Pig)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=21121490; PubMed=11229814;
 RA Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,
 RA Kim H.K.W.;
 RT "Porcine factor V: cDNA cloning, gene mapping, three-dimensional
 RT protein modeling of membrane binding sites and comparative anatomy of
 RT domains.";
 RL Cell. Mol. Life Sci. 58:148-159(2001).
 CC -!- FUNCTION: Protein C is a vitamin K-dependent serine protease that
 CC regulates blood coagulation by inactivating factors Va and VIIIa
 CC in the presence of calcium ions and phospholipids.
 CC -!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 CC and VIIIa
 CC -!- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
 CC into a light chain and a heavy chain held together by a disulfide
 CC bond. The enzyme is then activated by thrombin, which cleaves a
 CC tetradecapeptide from the amino end of the heavy chain; this
 CC reaction, which occurs at the surface of endothelial cells, is
 CC strongly promoted by thrombomodulin.
 CC -!- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
 CC residues allows the modified protein to bind calcium.
 CC -!- MISCELLANEOUS: Calcium also binds, with stronger affinity to
 CC another site, beyond the GLA domain. This GLA-independent binding
 CC site is necessary for the recognition of the thrombin-
 CC thrombomodulin complex.
 CC -!- SIMILARITY: Belongs to the peptidase S1 family.
 CC -!- SIMILARITY: Contains 2 EGF-like domains.
 CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (GLA)
 CC domain.
 CC -----
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 CC -----
 CC EMBL; AF191307; AAG28380.1; -.
 CC HSSP; P04070; 1AUT.
 CC -----
 CC MEROPS: S01.218; -.
 CC InterPro; IPR000152; Asx_hydroxyl_S.
 CC InterPro; IPR000742; EGF_2.
 CC InterPro; IPR001881; EGF_Ca.
 CC InterPro; IPR006209; EGF like.
 CC InterPro; IPR002383; GLA_blood.
 CC InterPro; IPR006210; IEGF.
 CC InterPro; IPR009003; Pept_Ser_Cys.
 CC InterPro; IPR001254; Peptidase_S1.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC InterPro; IPR002294; VitK_dep_GLA.
 CC Pfam; PF00008; EGF; 2.
 CC Pfam; PF00594; Gla; 1.
 CC Pfam; PF00089; Trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00001; GLABLOOD.
 CC SMART; SM00181; EGF; 2.
 CC SMART; SM00069; GLA; 1.
 CC SMART; SM00020; Tryp_Spc; 1.
 CC PROSITE; PS00010; ASX_HYDROXYL; 1.
 CC PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS00998; GLA_2; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Calcium-binding; EGF-like domain;
 KW Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;
 KW Repeat; Serine protease; Signal; Vitamin K.
 FT SIGNAL 1 18
 FT PROPEP 19 41
 FT CHAIN 42 459
 FT CHAIN 42 196
 FT CHAIN 199 459
 FT PEPTIDE 199 213
 FT SITE 213 214
 FT DOMAIN 42 87
 FT DOMAIN 96 131
 FT DOMAIN 135 175
 FT DOMAIN 214 459
 FT MOD_RES 47 47
 FT MOD_RES 48 48
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 FT MOD_RES 57 57
 FT MOD_RES 60 60
 FT MOD_RES 61 61
 FT MOD_RES 66 66
 FT MOD_RES 67 67
 FT MOD_RES 70 70
 FT MOD_RES 112 112
 FT ACT_SITE 255 255
 FT ACT_SITE 301 301
 FT ACT_SITE 400 400
 FT DISULFID 58 63
 FT DISULFID 91 110
 FT DISULFID 100 105
 FT DISULFID 104 119
 FT DISULFID 121 130
 FT DISULFID 139 150
 FT DISULFID 146 159
 FT DISULFID 161 174
 FT DISULFID 182 321
 FT DISULFID 240 256
 FT DISULFID 371 385
 FT DISULFID 396 424
 FT CARBOHYD 138 138
 FT CARBOHYD 292 292
 FT CARBOHYD 353 353
 SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;
 Query Match 52.3%; Score 103.5; DB 1; Length 459;
 Best Local Similarity 48.9%; Pred. No. 2.5e-09;
 Matches 22; Conservative 3; Mismatches 19; Indels 1; Gaps 1;
 Oy 1 ANAGFLXLRPGSLRXCKXQCSFXXARXIFKDXRTKLFWSY 45
 Db 42 ANS-FLBELRPSSLERCKBETCFEAREIFQNTENTMAFWSKY 85
 RESULT 8
 ID Q804X1 PRELIMINARY; PRT; 442 AA.
 AC Q804X1;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Coagulation factor VIIb (FC 3.4.21.21).
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 CC Tetraodontoidea; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RP [1]
 RN SEQUENCE FROM N.A.
 RA Davidson C.J., Hirt R.P., Lal K., Snell P., Elgar G.,
 RA Tuddenham E.G.D., McVey J.H.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to peptidase family S1.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 DR EMBL; AF465274; AAO33369.1; -.
 DR HSSP; P00740; 1CFH.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004283; F:chymotrypsin activity; IEA.
 DR GO; GO:0003802; F:coagulation factor VIIa activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR001314; Peptidase S1A.
 DR InterPro; IPR003003; Pept Ser Cys.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; Gla; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRYPSIN_DOM; 1.
 DR SMART; SM00020; TRYPSIN_DOM; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS00266; EGF_3; 1.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS0134; TRYPSIN_HIS; UNKNOWN_1.
 DR EGF-like domain; Hydrolase; Protease; Serine protease.
 KW EGF-like domain; Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 442 AA; 48787 MW; 810A561A127F0CE7 CRC64;

 Query Match 52.0%; Score 103; DB 2; Length 442;
 Best Local Similarity 40.0%; Pred. No. 3e-09;
 Matches 18; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

 Qy 1 ANAGFLXXLRPGSLXKXKXQCSFXXARXIFKDXRTKLFWSY 45
 Db 38 ANSGFLEMQGNLKRCEIBICNYEARVEFDDAQTKEWET 82

 RESULT 9
 Q804W8
 ID Q804W8 PRELIMINARY; PRT; 537 AA.
 AC Q804W8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Coagulation factor IX (EC 3.4.21.22).
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 CC Tetraodontoidea; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RP [1]
 RN SEQUENCE FROM N.A.
 RA Davidson C.J., Hirt R.P., Lal K., Snell P., Elgar G.,
 RA Tuddenham E.G.D., McVey J.H.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Belongs to peptidase family S1.
 DR EMBL; AF465277; AAO33372.1; -.
 DR HSSP; P00760; 1EZK.
 DR MEROPS; S01.215; -.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0003803; F:coagulation factor IXa activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR001314; Peptidase S1A.
 DR InterPro; IPR009003; Pept Ser Cys.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; Gla; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00179; EGF_Ca; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRYPSIN_DOM; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS01187; EGF_Ca; 1.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS0134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR EGF-like domain; Hydrolase; Protease; Serine protease.
 KW EGF-like domain; Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 537 AA; 60449 MW; ABD40ADPB7F23851 CRC64;

 Query Match 51.0%; Score 101; DB 2; Length 537;
 Best Local Similarity 40.9%; Pred. No. 8.1e-09;
 Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

 Qy 2 NAGFLXXLRPGSLXKXKXQCSFXXARXIFKDXRTKLFWSY 45
 Db 47 NSGHLEELQKNLERCKEEOCTMEAREVFEDDEKTAERFWGY 90

 RESULT 10
 PRTC MOUSE
 ID PRTC MOUSE STANDARD; PRT; 460 AA.
 AC P33587; O35498; Q91WN8; Q99PC6;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Vitamin K-dependent protein C precursor (EC 3.4.21.69)
 DE (Autoproteolysis IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).
 DE Name=Proc;
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=92316897; PubMed=1618739;
 RA Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;
 RT "Isolation and characterization of a mouse protein C cDNA.";
 RL J. Biochem. 111:491-495(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ;

RX MEDLINE=98152576; PubMed=9493582;
RA Jalbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,
RA Castellino F.J.;
RT "Nucleotide structure and characterization of the murine gene encoding
RT anticoagulant protein C";
RL Thromb. Haemost. 79:310-316(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Korf I.;
RT "Complete sequence of UC72A01";
RL Submitted (NOV-2000) to the EMBL/GenBank/DDSB databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 274-433 FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=94318474; PubMed=8043441;
RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
RT "A comparative study of partial primary structures of the catalytic
RT region of mammalian protein C";
RL Br. J. Haematol. 86:590-600(1994).
CC -!- FUNCTION: Protein C is a vitamin K-dependent serine protease that
CC regulates blood coagulation by inactivating factors Va and VIIIa
CC in the presence of calcium ions and phospholipids.
CC -!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIa.
CC -!- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
CC into a light chain and a heavy chain held together by a disulfide
CC bond. The enzyme is then activated by thrombin, which cleaves a
CC tetradecapeptide from the amino end of the heavy chain; this
CC reaction, which occurs at the surface of endothelial cells, is
CC strongly promoted by thrombomodulin.
CC -!- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
CC residues allows the modified protein to bind calcium.
CC -!- MISCELLANEOUS: Calcium also binds with stronger affinity to
CC another site, beyond the GLA domain. This GLA-independent binding
CC site is necessary for the recognition of the thrombin-
CC thrombomodulin complex.
CC -!- SIMILARITY: Belongs to the peptidase S1 family.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
CC domain.

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CC EMBL; D10445; BAA01235.1; --
DR EMBL; AF034569; AAC33795.1; --
DR EMBL; AF318182; AAK07918.1; --
DR EMBL; BC013896; AAHL3896.1; --
DR EMBL; D43755; BAA07812.1; --
DR PIR; JX0210; JX0210.
DR HSSP; P04070; LAUT.
DR MEROPS; S01.218; --
DR MGD; MGI:97771; PROC.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00008; VitK_dep_GLA.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS50998; GLA_2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Calcium-binding; EGF-like domain;
KW Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;
Repeat; Serine protease; Signal; Vitamin K.
FT SIGNAL; 1 33 By similarity.
FT PROPEP; 34 41 By similarity.
FT CHAIN; 42 460 Vitamin K-dependent protein C.
FT CHAIN; 42 196 Vitamin K-dependent protein C light chain
FT CHAIN; 199 460 (By similarity).
FT CHAIN; 199 460 Vitamin K-dependent protein C heavy chain
FT CHAIN; 199 460 (By similarity).
FT PEPTIDE; 199 212 Activation peptide (By similarity).
FT SITE; 212 213 Cleavage (by thrombin) (By similarity).
FT DOMAIN; 42 87 Gla.
FT DOMAIN; 96 131 EGF-like 1.
FT DOMAIN; 135 175 EGF-like 2.
FT DOMAIN; 213 460 Serine protease.
FT MOD_RES; 47 47 4-carboxyglutamate (By similarity).
FT MOD_RES; 48 48 4-carboxyglutamate (By similarity).
FT MOD_RES; 55 55 4-carboxyglutamate (By similarity).
FT MOD_RES; 57 57 4-carboxyglutamate (By similarity).
FT MOD_RES; 60 60 4-carboxyglutamate (By similarity).
FT MOD_RES; 61 61 4-carboxyglutamate (By similarity).
FT MOD_RES; 66 66 4-carboxyglutamate (By similarity).
FT MOD_RES; 67 67 4-carboxyglutamate (By similarity).
FT MOD_RES; 70 70 4-carboxyglutamate (By similarity).
FT MOD_RES; 112 112 3-hydroxyaspartate (By similarity).
FT ACT_SITE; 253 253 Charge relay system.
FT ACT_SITE; 299 299 Charge relay system.
FT ACT_SITE; 401 401 Charge relay system.
FT DISULFID; 58 63 By similarity.
FT DISULFID; 91 110 By similarity.
FT DISULFID; 100 105 By similarity.
FT DISULFID; 104 119 By similarity.
FT DISULFID; 121 130 By similarity.
FT DISULFID; 139 150 By similarity.

FT DISULFID 146 159 By similarity.
 FT DISULFID 161 174 By similarity.
 FT DISULFID 182 319 Interchain (By similarity).
 FT DISULFID 238 254 By similarity.
 FT DISULFID 397 425 By similarity.
 FT CARBOHYD 214 290 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 290 290 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 354 354 N-linked (GlcNAc...) (potential).
 FT VARIANT 327 327 Q -> Q (in strain BALB/c).
 FT VARIANT 392 392 D -> N (in strain BALB/c).
 FT CONFLICT 65 65 F -> L (in Ref. 3).
 SQ SEQUENCE 460 AA; 51818 MW; 0117F26E86FC274 CRC64;

 Query Match 49.7%; Score 98.5; DB 1; Length 460;
 Best Local Similarity 46.7%; Pred. No. 1.9e-06;
 Matches 21; Conservative 5; Mismatches 18; Indels 1; Gaps 1;

 QY 1 ANAGFLXXLRPGSLRXCKXXQCXFXRXRXIFKDXRTKLFWSY 45
 DB 42 ANS-FLEEMRPGSLRECMIEICDFEQAQEIFQNVDTLAFWKY 85

 RESULT 11
 TMG1 HUMAN
 ID TMG1 HUMAN STANDARD; PRT; 218 AA.
 AC O14658;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Transmembrane gamma-carboxyglutamic acid protein 1 precursor (Proline-rich Gla protein 1) (Proline-rich gamma-carboxyglutamic acid protein 1).
 DE 1).
 GN Name=PRG1; Synonyms=PRGP1, TMG1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97404347; PubMed=9256434; DOI=10.1073/pnas.94.17.9058;
 RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
 RT "Primary structure and tissue distribution of two novel proline-rich gamma-carboxyglutamic acid proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- TISSUE SPECIFICITY: Highly expressed in the spinal cord.
 CC -1- PWM: Gla residues are produced after subsequent posttranslational modifications of glutamate by a vitamin K-dependent gamma-carboxylase.

CC -1- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla) domain.
 CC -----
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 CC -----
 CC EMBL; AF009242; AAB67070.1; -;
 CC EMBL; BC060833; AAB60833.1; -;
 CC HSP; P00740; ICFH.
 CC Genew; HGNC:9469; PRRG1.
 CC MM; 604428; -;
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC InterPro; IPR002383; GLA_blood.
 CC InterPro; IPR000294; VitK_dep_GLA.
 CC Pfam; PF00594; Gla; 1.
 CC PRINTS; PR00001; GLABLOOD.
 CC SMART; SM00069; GLA; 1.
 CC PROSITE; PS00011; GLA_1; 1.
 CC PROSITE; PS00998; GLA_2; 1.
 CC Gamma-carboxyglutamic acid; Transmembrane; Vitamin K.
 FT PROPEP 1 20 Potential.
 FT CHAIN 21 218 Transmembrane gamma-carboxyglutamic acid protein 1.
 FT DOMAIN 21 83 Extracellular (Potential).
 FT TRANSMEM 84 106 Potential.
 FT DOMAIN 107 218 Cytoplasmic (Potential).
 FT DOMAIN 21 66 Gla.
 FT DOMAIN 131 135 Poly-Pro.
 SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AEB98 CRC64;

 Query Match 48.0%; Score 95; DB 1; Length 218;
 Best Local Similarity 40.5%; Pred. No. 3.8e-08;
 Matches 17; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

 QY 4 GFLXLRPGSLRXCKXQCSXRXRXIFKDXRTKLFWSY 45
 DB 23 GPFEEIRQGNIECKEECTFEAREAFENNEKTFEWSY 64

 RESULT 12
 Q8NEK6
 ID Q8NEK6 PRELIMINARY; PRT; 266 AA.
 AC Q8NEK6;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE PRRG1 protein (Fragment).
 GN Name=PRRG1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030786; AAH30786.2; -;
DR HSP; P00740; ICFH.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; Gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLA 1; 1.
FT NON TER 1
SQ SEQUENCE 266 AA; 30151 MW; 175768024D635351 CRC64;
Query Match 48.0%; Score 95; DB 2; Length 266;
Best Local Similarity 40.5%; Pred. No. 4.6e-08;
Matches 17; Conservative 8; Mismatches 17; Indels 0; Gaps 0;
QY 4 GFLXXLRGSLRXCKXQCSPXXARXIFPKDAXRKLFWISY 45
DB 71 GFPEIRQNIREEKEEFCTFEAREAPENNEKTFWSTY 112
RESULT 13
THRB_RAT
ID THRB_RAT STANDARD; PRT; 617 AA.
AC P18292;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Prothrombin precursor (EC 3.4.21.5).
GN Name=P2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RA MEDLINE=90332426; PubMed=2377469;
RA Dihanich M., Monard D.;
RT "cDNA sequence of rat prothrombin.";
RL Nucleic Acids Res. 18:4251-4251(1990).
RN [2]
RP SEQUENCE OF 383-617 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=9221913; PubMed=1557383;
RA Banfield D.K., McGillivray R.T.;
RT "Partial characterization of vertebrate prothrombin cDNAs:
RT amplification and sequence analysis of the B chain of thrombin from
RT nine different species.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
CC -1- FUNCTION: Thrombin, which cleaves bonds after Arg and Lys,
CC converts fibrinogen to fibrin and activates factors V, VII, VIII,
CC XIII, and, in complex with thrombomodulin, protein C.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Gly; activates
CC fibrinogen to fibrin and releases fibrinopeptide A and B.
CC -1- PTM: The gamma-carboxyglutamyl residues, which bind calcium ions,
CC result from the carboxylation of glutamyl residues by a microsomal
CC enzyme, the vitamin K-dependent carboxylase. The modified residues
CC are necessary for the calcium-dependent interaction with a

negatively charged phospholipid surface, which is essential for
the conversion of prothrombin to thrombin.
-1- MISCELLANEOUS: Prothrombin is activated on the surface of a
phospholipid membrane that binds the amino end of prothrombin and
factors Va and Xa in Ca-dependent interactions; factor Xa removes
the activation peptide and cleaves the remaining part into light
and heavy chains. The activation process starts slowly because
factor V itself has to be activated by the initial, small amounts
of thrombin.
-1- MISCELLANEOUS: Thrombin can itself cleave the amino terminal
fragment (fragment 1) of the prothrombin, prior to its activation
by factor Xa.
-1- SIMILARITY: Belongs to the peptidase S1 family.
-1- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
domain.
-1- SIMILARITY: Contains 2 kringle domains.

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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL; X52835; CAA37017.1; -;
DR EMBL; M81397; AAA42240.1; -;
DR PIR; S10511; S10511.
DR HSP; P00734; 1UVS.
DR MEROPS; S01-217; -;
DR RGD; 61996; F2.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR009003; Pept Ser Cys.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR003966; Peptidase_S1A_pr.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00051; Kringle; 2.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00130; KR; 2.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS50998; GLA_2; 1.
DR PROSITE; PS00021; KRINGLE_1; 2.
DR PROSITE; PS50070; KRINGLE_2; 2.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Acute phase; Blood coagulation; Calcium-binding;
KW Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Kringle; Plasma;
KW Repeat; Serine protease; Signal; Vitamin K; Zymogen.
FT SIGNAL 1 24 Potential.
FT PROPEP 25 43
FT CHAIN 44 617 Prothrombin.
FT PEPTIDE 44 200 Activation peptide (fragment 1).
FT PEPTIDE 201 323 Activation peptide (fragment 2).
FT CHAIN 324 359 Thrombin light chain.
FT CHAIN 360 617 Thrombin heavy chain.
FT DOMAIN 44 90 Gla.
FT DOMAIN 109 187 Kringle 1.
FT DOMAIN 215 292 Kringle 2.
FT DOMAIN 360 617 Serine protease.
FT SITE 200 201 Cleavage (by thrombin).
FT SITE 323 324 Cleavage (by factor Xa).
FT SITE 359 360 Cleavage (by factor Xa).

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FT ACT SITE 402 Charge relay system (By similarity).
FT ACT SITE 458 Charge relay system (By similarity).
FT ACT SITE 564 Charge relay system (By similarity).
FT MOD_RES 50 4-carboxyglutamate.
FT MOD_RES 51 4-carboxyglutamate.
FT MOD_RES 58 4-carboxyglutamate.
FT MOD_RES 60 4-carboxyglutamate.
FT MOD_RES 63 4-carboxyglutamate.
FT MOD_RES 64 4-carboxyglutamate.
FT MOD_RES 69 4-carboxyglutamate.
FT MOD_RES 70 4-carboxyglutamate.
FT MOD_RES 73 4-carboxyglutamate.
FT MOD_RES 76 4-carboxyglutamate.
FT CARBOHYD 120 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 144 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 412 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 552 N-linked (GlcNAc... ) (Potential).
FT DISULFID 61 By similarity.
FT DISULFID 91 By similarity.
FT DISULFID 109 By similarity.
FT DISULFID 130 By similarity.
FT DISULFID 158 By similarity.
FT DISULFID 215 By similarity.
FT DISULFID 236 By similarity.
FT DISULFID 264 By similarity.
FT DISULFID 332 Interchain (By similarity).
FT DISULFID 387 By similarity.
FT DISULFID 532 By similarity.
FT DISULFID 560 By similarity.
SQ SEQUENCE 617 AA; 70411 MW; AD27DB171445DB1D CRC64;

Query Match 48.0%; Score 95; DB 1; Length 617;
Best Local Similarity 42.2%; Pred. No. 1.1e-07;
Matches 19; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANAGFLXXLRGSLXKXQXQXFFXARXIFKDXRTKLFWSY 45
Db 44 ANSGFLBRLKGNLERECVBEQCSYEFAPFALESPOQTDVFWAKY 88

RESULT 14
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ID -THRB MOUSE STANDARD; PRT; 618 AA.
AC P19221;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Prothrombin precursor (EC 3.4.21.5).
GN Name=F2; Synonyms=Cf2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Liver;
RX MEDLINE=91025551; PubMed=2222810;
RA Friezen Degen S.J.; Schaffer L.A.; Jamison C.S.; Grant S.G.;
RA Fitzgibbon J.J.; Pai J.-A.; Chapman V.W.; Elliott R.W.;
RT "Characterization of the cDNA coding for mouse prothrombin and
RL localization of the gene on mouse chromosome 2.";
RN DNA Cell Biol. 9:487-498(1990).
[2]
SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=22388257; PubMed=24277932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Haieh F.;
RA Diatchenko L.; Narusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
RA Brownstein M.J.; Ustin T.B.; Toshiyuki S.; Carninci P.; Prange C.,

```

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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Warra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
SEQUENCE OF 384-618 FROM N.A.
TISSUE=Liver;
MEDLINE=92212913; PubMed=1557383;
RA Banfield D.K., Macgillivray R.T.;
RT "Partial characterization of vertebrate prothrombin cDNAs:
RT amplification and sequence analysis of the B chain of thrombin from
RT nine different species.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
CC -I- FUNCTION: Thrombin, which cleaves bonds after Arg and Lys,
CC converts fibrinogen to fibrin and activates factors V, VII, VIII,
CC XIII, and, in complex with thrombomodulin, protein C.
CC -I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-[Gly; activates
CC fibrinogen to fibrin and releases fibrinopeptide A and B.
CC -I- PTM: The gamma-carboxyglutamyl residues, which bind calcium ions,
CC result from the carboxylation of glutamyl residues by a microsomal
CC enzyme, the vitamin K-dependent carboxylase. The modified residues
CC are necessary for the calcium-dependent interaction with a
CC negatively charged phospholipid surface, which is essential for
CC the conversion of prothrombin to thrombin.
CC -I- MISCELLANEOUS: Prothrombin is activated on the surface of a
CC phospholipid membrane that binds the amino end of prothrombin and
CC factors Va and Xa in Ca-dependent interactions; factor Xa removes
CC the activation peptide and cleaves the remaining part into light
CC and heavy chains. The activation process starts slowly because
CC factor V itself has to be activated by the initial, small amounts
CC of thrombin.
CC -I- MISCELLANEOUS: Thrombin can itself cleave the amino terminal
CC fragment (fragment 1) of the prothrombin, prior to its activation
CC by factor Xa.
CC -I- SIMILARITY: Belongs to the peptidase S1 family.
CC -I- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
CC domain.
CC -I- SIMILARITY: Contains 2 kringle domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/ebis/announcement/
CC or send an email to license@ebi.ac.uk).
CC -----
CC ENBL; X52308; CAA36548.1; -.
CC DR ENBL; BC013662; AAH13662.1; -.
CC DR ENBL; M81394; AAA0435.1; -.
CC DR PIR; A35827; A35827.
CC DR HSSP; P00734; 1B7X.
CC DR MEROPS; S01.217; -.
CC DR MGD; MGI:88380; F2.
CC DR InterPro; IPR002383; GLA_blood.
CC DR InterPro; IPR000001; Kringle.
CC DR InterPro; IPR009003; Pept_Ser_Cys.
CC DR InterPro; IPR001254; Peptidase_S1.
CC DR InterPro; IPR001314; Peptidase_S1A.
CC DR InterPro; IPR003966; Peptidase_S1A_pr.
CC DR InterPro; IPR000294; VitK_dep_GLA.
CC DR Pfam; PF00594; Gla; 1.
CC DR Pfam; PF00051; Kringle; 2.
CC DR Pfam; PF00089; Trypsin; 1.

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DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00998; GLA_2; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Calcium-binding; EGF-like domain;
KW Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;
KW Plasma; Repeat; Serine protease; Signal; Vitamin K; Zymogen.
FT SIGNAL 1 24 Potential.
FT PROPEP 25 41 Potential.
FT CHAIN 42 193 Factor VII light chain (By similarity).
FT CHAIN 194 446 Factor VII heavy chain (By similarity).
FT DOMAIN 42 86 Gla.
FT DOMAIN 87 123 EGF-like 1, calcium-binding (Potential).
FT DOMAIN 128 169 EGF-like 2.
FT DOMAIN 194 446 Serine protease.
FT SITE 193 194 Cleavage (by factor Xa, factor XIIa,
FT ACT_SITE 234 234 factor IXa, or thrombin) (By similarity).
FT ACT_SITE 283 283 By similarity.
FT ACT_SITE 385 385 By similarity.
FT BINDING 379 379 Substrate (By similarity).
FT DISULFID 58 63 By similarity.
FT DISULFID 91 102 By similarity.
FT DISULFID 96 111 By similarity.
FT DISULFID 113 122 By similarity.
FT DISULFID 132 143 By similarity.
FT DISULFID 139 153 By similarity.
FT DISULFID 155 168 By similarity.
FT DISULFID 176 303 By similarity.
FT DISULFID 200 205 By similarity.
FT DISULFID 219 235 By similarity.
FT DISULFID 351 370 By similarity.
FT DISULFID 381 409 By similarity.
FT MOD_RES 47 47 4-carboxyglutamate (By similarity).
FT MOD_RES 48 48 4-carboxyglutamate (By similarity).
FT MOD_RES 55 55 4-carboxyglutamate (By similarity).
FT MOD_RES 57 57 4-carboxyglutamate (By similarity).
FT MOD_RES 60 60 4-carboxyglutamate (By similarity).
FT MOD_RES 61 61 4-carboxyglutamate (By similarity).
FT MOD_RES 66 66 4-carboxyglutamate (By similarity).
FT MOD_RES 67 67 4-carboxyglutamate (By similarity).
FT MOD_RES 70 70 4-carboxyglutamate (By similarity).
FT MOD_RES 76 76 4-carboxyglutamate (By similarity).
FT MOD_RES 104 104 3-hydroxyaspartate (By similarity).
FT CARBOHYD 186 186 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 244 244 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 446 AA; 50399 MW; 292985EBF119C0AA CRC64;
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Query Match 47.2%; Score 93.5; DB 1; Length 446;
Best Local Similarity 48.9%; Pred. No. 1.4e-07;
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Matches 22; Conservative 2; Mismatches 20; Indels 1; Gaps 1;
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Qy 1 ANAGFLXXLRPGSLRXKXXQCSFXXARXIFKDXFTKLFWSY 45
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Db 42 ANS-LLEELWSSSLERECEERCSFEARIFKSPERTKQFTIY 85
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Search completed: August 22, 2005, 18:42:26
Job time : 84 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	161.5	81.6	44	3	US-08-955-636-3	Sequence 3, Appli
2	161.5	81.6	44	4	US-09-102-239-3	Sequence 3, Appli
3	161.5	81.6	44	4	US-09-357-591-3	Sequence 3, Appli
4	161.5	81.6	44	4	US-09-803-810-3	Sequence 3, Appli
5	161.5	81.6	406	1	US-08-293-778-24	Sequence 24, Appli
6	161.5	81.6	406	1	US-08-955-411-5	Sequence 5, Appli
7	161.5	81.6	406	2	US-08-995-471-5	Sequence 5, Appli
8	161.5	81.6	406	4	US-09-782-587B-1	Sequence 1, Appli
9	161.5	81.6	406	4	US-09-782-587B-3	Sequence 3, Appli
10	161.5	81.6	406	5	PCT-US92-10242-5	Sequence 5, Appli
11	161.5	81.6	444	1	US-08-475-845-2	Sequence 2, Appli
12	161.5	81.6	444	2	US-08-327-690-2	Sequence 2, Appli
13	161.5	81.6	444	2	US-08-660-289-2	Sequence 2, Appli
14	161.5	81.6	444	2	US-08-537-807-2	Sequence 2, Appli
15	161.5	81.6	444	2	US-08-871-003-2	Sequence 2, Appli
16	161.5	81.6	444	3	US-08-464-233-2	Sequence 2, Appli
17	161.5	81.6	444	3	US-09-189-607-2	Sequence 2, Appli
18	161.5	81.6	444	3	US-09-378-907-2	Sequence 2, Appli
19	161.5	81.6	444	5	PCT-US94-05779-2	Sequence 2, Appli
20	161.5	81.6	461	4	US-09-949-016-8839	Sequence 8839, Ap
21	161.5	81.6	466	1	US-07-882-202A-4	Sequence 4, Appli
22	161.5	81.6	466	1	US-08-021-615A-4	Sequence 4, Appli
23	161.5	81.6	466	1	US-08-321-777-4	Sequence 4, Appli
24	161.5	81.6	466	3	US-09-009-217-14	Sequence 14, Appl
25	161.5	81.6	466	3	US-09-009-656-14	Sequence 14, Appl
26	161.5	81.6	466	5	PCT-US93-04493-4	Sequence 4, Appli
27	161.5	81.6	483	4	US-09-949-016-9523	Sequence 9523, Ap

; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-09-302-239-3

Query Match 81.6%; Score 161.5; DB 4; Length 44;
Best Local Similarity 97.8%; Pred. No. 5.8e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXLRPGSLXRCXKXQCSFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLXLRPGSLXRCXKXQCSFXXARXIFKDXRTKLFWISY 44

RESULT 3
US-09-497-591-3
; Sequence 3, Application US/09497591
; Patent No. 6747003
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary L.
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531-016001
; CURRENT APPLICATION NUMBER: US/09/497,591
; CURRENT FILING DATE: 2000-02-03
; EARLIER APPLICATION NUMBER: 09/302,239
; EARLIER FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: 08/955,636
; EARLIER FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-09-497-591-3

Query Match 81.6%; Score 161.5; DB 4; Length 44;
Best Local Similarity 97.8%; Pred. No. 5.8e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXLRPGSLXRCXKXQCSFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLXLRPGSLXRCXKXQCSFXXARXIFKDXRTKLFWISY 44

RESULT 4
US-09-803-810-3
; Sequence 3, Application US/09803810
; Patent No. 6762286
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary L.
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/09/803,810
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-09-803-810-3

Query Match 81.6%; Score 161.5; DB 4; Length 44;
Best Local Similarity 97.8%; Pred. No. 5.8e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXLRPGSLXRCXKXQCSFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLXLRPGSLXRCXKXQCSFXXARXIFKDXRTKLFWISY 44

RESULT 5
US-08-293-778-24
; Sequence 24, Application US/08293778
; Patent No. 5580560
; GENERAL INFORMATION:
; APPLICANT: Nicolaisen, Else M.
; APPLICANT: Bjorn, Soren E.
; APPLICANT: Wiberg, Finn C.
; APPLICANT: Woodbury, Richard
; TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,778
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/104,509
; FILING DATE:
; APPLICATION NUMBER: DK 3235/87
; FILING DATE: 25-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/434,149
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK88/00103
; FILING DATE: 24-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,248
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Agria, Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 3129.224-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-293-778-24

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Best Local Similarity 75.6%; Pred. No. 5.8e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAGFLXLRPGSLXRCXKXQCSFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLYLRPGSLYRCYKCYQCSFYARYIFKDAYRTKLFWISY 44

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; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,471
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/295,411
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
; US-08-955-471-5
;
; Query Match 81.6%; Score 161.5; DB 2; Length 406;
; Best Local Similarity 75.6%; Pred. No. 5.8e-19;
; Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
;
; QY 1 ANAGFLXLRPGSLXKXCKXKXOCSPXXARXIFKDXARTKLFWISY 45
; ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
;
; Db 1 ANA-FLEELRPGSLRECKEEQCSFEAREIFKDAERTKLFWISY 44
;
;
; RESULT 8
; US-09-782-587B-1
; Sequence 1, Application US/09782587B
; Patent No. 6806063
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26

```

;; PRIOR APPLICATION NUMBER: PA 2000 00218
;; PRIOR FILING DATE: 2000-02-11
;; PRIOR APPLICATION NUMBER: 60/184,036
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: 60/241,916
;; PRIOR FILING DATE: 2000-10-18
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)-(7)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (14)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (16)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (19)..(20)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (25)-(26)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (29)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (35)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
US-09-782-587B-1

Query Match 81.6%; Score 161.5; DB 4; Length 406;
Best Local Similarity 97.8%; Pred. No. 5.8e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXLRPGSLXRXCKXQCQSFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLXLRPGSLXRXCKXQCQSFXXARXIFKDXRTKLFWISY 44

RESULT 9
US-09-782-587B-3
; Sequence 3, Application US/09782587B
; Patent No. 6806063
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAU
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-587B-3

Query Match 81.6%; Score 161.5; DB 4; Length 406;
Best Local Similarity 75.6%; Pred. No. 5.8e-19;

Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
Qy 1 ANAGFLXLRPGSLXRXCKXQCQSFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLXLRPGSLXRXCKXQCQSFXXARXIFKDXRTKLFWISY 44
RESULT 10
PCT-US92-10242-5
; Sequence 5, Application PC/TUS9210242
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 North Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10242
; FILING DATE: 19921118
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRO472P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
PCT-US92-10242-5

Query Match 81.6%; Score 161.5; DB 5; Length 406;
Best Local Similarity 75.6%; Pred. No. 5.8e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAGFLXLRPGSLXRXCKXQCQSFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLXLRPGSLXRXCKXQCQSFXXARXIFKDXRTKLFWISY 44

RESULT 11
US-08-475-845-2

```

; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,690
; FILING DATE: 24-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-327-690-2

Query Match 81.6%; Score 161.5; DB 2; Length 4
Best Local Similarity 75.8%; Pred. No. 6.3e-19;
Matches 34; Conservative 0; Mismatches 10; Indels

QY 1 ANAGFLXLRPSGLXRXKXKXCSFXXARXKPKDAXRTKLFWISY 45
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39 ANA-FLELRPSGLRECKEEOCSFEAREIFKDAERTKLFWISY 82
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
US-08-660-289-2
; Sequence 2, Application US/08660289
; Patent No. 5833982
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.24

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	161.5	81.6	44	9	US-09-803-810-3	Sequence 3
2	161.5	81.6	44	14	US-10-298-330-3	Sequence 1
3	161.5	81.6	44	16	US-10-855-068-3	Sequence 1
4	161.5	81.6	406	10	US-09-783-587B-1	Sequence 1
5	161.5	81.6	406	10	US-09-782-587B-3	Sequence 1
6	161.5	81.6	406	14	US-10-109-498-1	Sequence 1
7	161.5	81.6	406	14	US-10-255-032-1	Sequence 1
8	161.5	81.6	406	14	US-10-281-727-1	Sequence 1
9	161.5	81.6	406	15	US-10-386-898-7	Sequence 1
10	161.5	81.6	406	15	US-10-383-898-1	Sequence 1
11	161.5	81.6	406	15	US-10-617-500-1	Sequence 1

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; Sequence 3, Application US/10298330
; Publication No. US20030100506A1
; GENERAL INFORMATION:
; APPLICANT: Nelstuen, Gary L.
; TITLE OF INVENTION: Modified Vitamin K-Dependent
; FILE REFERENCE: 09531-127001
; CURRENT APPLICATION NUMBER: US/10/298,330
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/497,591
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/302,239
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 08/955,636
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 35
; OTHER INFORMATION: xaa = gamma carboxyglutamic acid or glutamic acid
US-10-298-330-3

Query Match      81.6%; Score 161.5; DB 14; Length 44;
Best Local Similarity 97.8%; Pred. No. 1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy      1 ANAGFLXXLRPGSLXRXCKXQCQCFXXARXIFKDXARTKLFWISY 45
Db      1 ANA-FLXXLRPGSLXRXCKXQCQCFXXARXIFKDXARTKLFWISY 44

RESULT 3
US-10-855-068-3
; Sequence 3, Application US/10855068
; Publication No. US20040220106A1
; GENERAL INFORMATION:
; APPLICANT: Nelstuen, Gary L.
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/10/855,068
; CURRENT FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: US/09/302,239
; PRIOR FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: xaa=gamma carboxyglutamic acid or glutamic acid
US-10-855-068-3

Query Match      81.6%; Score 161.5; DB 16; Length 44;
Best Local Similarity 97.8%; Pred. No. 1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy      1 ANAGFLXXLRPGSLXRXCKXQCQCFXXARXIFKDXARTKLFWISY 45
Db      1 ANA-FLXXLRPGSLXRXCKXQCQCFXXARXIFKDXARTKLFWISY 44

RESULT 4
US-09-782-587B-1
; Sequence 1, Application US/09782587B
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; Publication No. US20030096338A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)..(7)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (14)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (16)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (19)..(20)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (25)..(26)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (29)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (35)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
US-09-782-587B-1

Query Match      81.6%; Score 161.5; DB 10; Length 406;
Best Local Similarity 97.8%; Pred. No. 9.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy      1 ANAGFLXXLRPGSLXRXCKXQCQCFXXARXIFKDXARTKLFWISY 45
Db      1 ANA-FLXXLRPGSLXRXCKXQCQCFXXARXIFKDXARTKLFWISY 44

RESULT 5
US-09-782-587B-3
; Sequence 3, Application US/09782587B
; Publication No. US20030096338A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
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; LOCATION: (1) : (406)
; OTHER INFORMATION: Xaa means 4-carboxylutamic acid (gamma-carboxylutamate)

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; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(406)
; OTHER INFORMATION: Xaa=4-carboxyglutamic acid (gamma-carboxyglutamate)
US-10-617-619-1

Query Match      81.6%; Score 161.5; DB 16; Length 406;
Best Local Similarity 97.8%; Pred. No. 9.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLXRXCKXXQCSPXXARXIFKDXARTKLFWISY 45
Db 1 ANA-FLXXLRPGSLXRXCKXXQCSPXXARXIFKDXARTKLFWISY 44

RESULT 14
US-10-701-294-1
; Sequence 1, Application US/10701294
; Publication No. US20040143099A1
; GENERAL INFORMATION:
; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
; APPLICANT: Petersen, Lars C
; APPLICANT: Back, Jakob M
; APPLICANT: Meyer, Christian
; TITLE OF INVENTION: Pharmaceutical Composition Comprising a Tissue Factor Antagonist
; FILE REFERENCE: 6608.200-US
; CURRENT APPLICATION NUMBER: US/10/701,294
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: US 60/434,904
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01710
; PRIOR FILING DATE: 2002-11-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: human coagulation Factor VII
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(406)
; OTHER INFORMATION: Xaa=4-carboxyglutamic acid (gamma-carboxyglutamate)
US-10-701-294-1

Query Match      81.6%; Score 161.5; DB 16; Length 406;
Best Local Similarity 97.8%; Pred. No. 9.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLXRXCKXXQCSPXXARXIFKDXARTKLFWISY 45
Db 1 ANA-FLXXLRPGSLXRXCKXXQCSPXXARXIFKDXARTKLFWISY 44

RESULT 15
US-10-669-537-1
; Sequence 1, Application US/10669537
; Publication No. US20040192602A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; APPLICANT: Olsen, Ole Hvilsted
; TITLE OF INVENTION: Human Coagulation Factor VII Polypeptides
; FILE REFERENCE: 6544.200-US
; CURRENT APPLICATION NUMBER: US/10/669,537
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01423
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 60/417,927
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 13
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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(406)
; OTHER INFORMATION: Xaa=carboxyglutamic acid (gamma-carboxyglutamate)
US-10-669-537-1

Query Match      81.6%; Score 161.5; DB 16; Length 406;
Best Local Similarity 97.8%; Pred. No. 9.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLXRXCKXXQCSPXXARXIFKDXARTKLFWISY 45
Db 1 ANA-FLXXLRPGSLXRXCKXXQCSPXXARXIFKDXARTKLFWISY 44

Search completed: August 22, 2005, 19:20:43
Job time : 662 secs
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OM protein - protein search, using sw model

Run on: August 22, 2005, 09:28:04 ; Search time 92 Seconds
(without alignments)
189.176 Million cell updates/sec

Title: US10031005-3Y4

Perfect score: 199

Sequence: 1 ANAYFLXLRPGSLXRXCX.....XXARXIFKDXRTKLFWISY 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	169	84.9	408	7	ADf44980 Human Fac
2	161.5	81.2	44	2	AAY18305 Human fac
3	161.5	81.2	44	4	AAB36395 Human fac
4	161.5	81.2	44	7	ADD50096 Human vit
5	161.5	81.2	44	8	ADQ26902 Human fac
6	161.5	81.2	401	4	AAB84870 Mutant bl
7	161.5	81.2	401	4	AAB84871 Mutant bl
8	161.5	81.2	406	2	AAR35764 Factor VI
9	161.5	81.2	406	2	AAW14510 Modified
10	161.5	81.2	406	2	AAW14509 Modified
11	161.5	81.2	406	4	Aau77745 Human fac
12	161.5	81.2	406	4	AAB84867 Mutant bl
13	161.5	81.2	406	4	AAB84868 Mutant bl
14	161.5	81.2	406	4	AAB84869 Mutant bl
15	161.5	81.2	406	4	AAB84866 Wild-type
16	161.5	81.2	406	4	AAM52183 Human FVI
17	161.5	81.2	406	4	AAM52172 Mammalian
18	161.5	81.2	406	4	AAM52186 Human FVI
19	161.5	81.2	406	4	AAM52171 Human FVI
20	161.5	81.2	406	4	AAM52187 Human FVI
21	161.5	81.2	406	4	AAM52181 Human FVI
22	161.5	81.2	406	4	AAM52185 Human FVI
23	161.5	81.2	406	4	AAM52184 Human FVI
24	161.5	81.2	406	4	AAM52182 Human FVI
25	161.5	81.2	406	5	AAU77196 Human coa

26	161.5	81.2	406	5	AAU77191 Human coa
27	161.5	81.2	406	5	AAU77200 Human coa
28	161.5	81.2	406	5	AAU77192 Human coa
29	161.5	81.2	406	5	AAU77190 Human coa
30	161.5	81.2	406	5	AAU77198 Human coa
31	161.5	81.2	406	5	AAU77193 Human coa
32	161.5	81.2	406	5	AAU77199 Human coa
33	161.5	81.2	406	5	AAU79201 Human coa
34	161.5	81.2	406	5	AAU77188 Human coa
35	161.5	81.2	406	5	AAU77194 Human coa
36	161.5	81.2	406	5	AAU77195 Human coa
37	161.5	81.2	406	5	AAU77189 Human coa
38	161.5	81.2	406	5	AAU77197 Human coa
39	161.5	81.2	406	5	ABG31688 Human coa
40	161.5	81.2	406	5	ABB09178 Human fac
41	161.5	81.2	406	5	ABB80051 Human coa
42	161.5	81.2	406	5	ABB80069 Human coa
43	161.5	81.2	406	5	ABB80072 Human coa
44	161.5	81.2	406	5	ABB80071 Human coa
45	161.5	81.2	406	5	ABB80068 Human coa

ALIGNMENTS

RESULT 1
ADf44980
ID ADf44980 standard; protein; 408 AA.
XX
AC ADf44980;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human Factor VII variant, A3AY.
XX
KW Human; Factor VII; FVII; Factor VIIa; FVIIa; blood coagulation factor;
KW blood clotting disorder; brain haemorrhage; trauma; bleeding;
KW Haemostatic.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 4..5 /note= "Residues AY were inserted after position 3"
XX
PN WO2003093465-A1.
XX
PD 13-NOV-2003.
XX
PF 29-APR-2003; 2003WO-DK000276.
XX
PR 30-APR-2002; 2002US-0376679P.
XX
FA (MAXY-) MAXYGEN APS.
FA (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI Haaning JM, Andersen KV, Pedersen AH;
XX
DR WPI; 2003-903672/82.
XX
PT New Factor VII (FVII) or Factor VIIa (FVIIa) polypeptide variant, useful
PT in preparing a composition for treating a disorder where clot formation
PT is desirable, e.g., brain hemorrhages or blunt or penetrative trauma.
XX
PS Claim 13; Page; 78pp; English.
XX
CC The present invention relates to novel variants of Factor VII (FVII) or
CC Factor VIIa (FVIIa) protein. FVII is a blood coagulation factor. The
CC present sequence is a variant of the invention. The variants are useful
CC in preparing a composition for treating a disorder where clot formation
CC is desirable, e.g., brain haemorrhages, blunt or penetrative trauma, or
CC bleeding in patients undergoing living transplantations or resection or

```
CC variceal bleedings. Note: The present sequence is not shown in the
CC specification, but was derived from information given in the wild-type
CC human FVII sequence (ADP44971) and Claim 13.
XX
SQ Sequence 408 AA;

Query Match      84.9%; Score 169; DB 7; Length 408;
Best Local Similarity 76.7%; Pred. No. 3.6e-20;
Matches 33; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy  3 AYFLXLLRPGSLRXCKXXQCFSXXARXIFKDXARTKLFWISY 45
    ||||| ||||| || ||||| ||||| ||||| ||||| |||||
Db  4 AYFLEELRPGSLRECKEQCSFEAREIFKDXARTKLFWISY 46
    ||||| ||||| || ||||| ||||| ||||| ||||| |||||

RESULT 2
AAY18305
ID  AAY18305 standard; peptide; 44 AA.
XX
AC  AAY18305;
XX
DT  17-AUG-1999 (first entry)
XX
DE  Human factor VII GLA domain.
XX
KW  GLA domain; vitamin K-dependent protein; clotting disorder; therapy.
XX
OS  Homo sapiens.
XX
FH  Key Location/Qualifiers
FT  Misc-difference 1..44
FT  /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
FT  acid"
XX
PN  WO9920767-A1.
XX
PD  29-APR-1999.
XX
PF  20-OCT-1998; 98WO-US022152.
XX
PR  23-OCT-1997; 97US-00955636.
XX
PA  (MINU ) UNIV MINNESOTA.
XX
PI  Nelsestuen GL;
XX
DR  WPI; 1999-288309/24.
XX
PT  Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid
PT  domain, useful for treating clotting disorders.
XX
PS  Disclosure; Page 15; 86pp; English.
XX
CC  This sequence is the factor VII GLA (gamma-carboxyglutamic acid) domain.
CC  The invention relates to a vitamin K-dependent polypeptide comprising a
CC  modified GLA domain containing an amino acid substitution which enhances
CC  membrane binding of the modified polypeptide as compared to the native
CC  polypeptide. The polypeptide is used to treat a clotting disorder by
CC  decreasing or increasing clot formation. Modification of the GLA domain
CC  results in a protein which has enhanced membrane binding affinity as
CC  compared to the native protein
XX
SQ Sequence 44 AA;

Query Match      81.2%; Score 161.5; DB 2; Length 44;
Best Local Similarity 97.8%; Pred. No. 7.2e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy  1 ANAYFLXLLRPGSLRXCKXXQCFSXXARXIFKDXARTKLFWISY 45
    ||||| ||||| || ||||| ||||| ||||| ||||| |||||
Db  1 ANA-FLXLLRPGSLRXCKXXQCFSXXARXIFKDXARTKLFWISY 44
    ||||| ||||| || ||||| ||||| ||||| ||||| |||||

RESULT 3
AAB36395
ID  AAB36395 standard; peptide; 44 AA.
XX
AC  AAB36395;
XX
DT  27-FEB-2001 (first entry)
XX
DE  Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
XX
KW  Vitamin K-dependent protein; factor VII; protein C; GLA domain;
KW  gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
KW  factor X; prothrombin; enhanced membrane binding affinity;
KW  clot formation; thrombolytic; haemostatic; bleeding disorder; thrombosis;
KW  clotting disorder; haemophilia A; haemophilia B; liver disease.
XX
OS  Homo sapiens.
XX
PN  WO20006753-A2.
XX
PD  09-NOV-2000.
XX
PF  28-APR-2000; 2000WO-US011416.
XX
PR  29-APR-1999; 99US-00302239.
XX
PA  (MINU ) UNIV MINNESOTA.
XX
PI  Nelsestuen GL;
XX
DR  WPI; 2001-007226/01.
XX
PT  Novel vitamin K-dependent polypeptide useful for treating clotting
PT  disorders such as thrombosis and hemophilia, comprises modified gamma-
PT  carboxy glutamic acid domain that enhances membrane binding affinity.
XX
PS  Disclosure; Page 12; 81pp; English.
XX
CC  The present invention describes a vitamin K-dependent polypeptide (I)
CC  comprising a modified gamma-carboxy glutamic acid (GLA) domain having at
CC  least one amino acid substitution, that enhances membrane binding
CC  affinity and the activity of the polypeptide relative to a corresponding
CC  native vitamin K-dependent polypeptide and inhibits clot formation. (I)
CC  can have thrombolytic and haemostatic activities, and can be used as an
CC  inhibitor of clot formation. (I) is useful for decreasing clot formation
CC  in a mammal, a factor VII or factor IX containing a modified GLA domain
CC  is useful for increasing clot formation and for treating a bleeding
CC  disorder, including thrombosis and clotting disorders such as haemophilia
CC  A, haemophilia B and liver disease. The present sequence represents a
CC  wild type human factor VII GLA domain sequence, given in the
CC  exemplification of the present invention
XX
SQ Sequence 44 AA;

Query Match      81.2%; Score 161.5; DB 4; Length 44;
Best Local Similarity 97.8%; Pred. No. 7.2e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy  1 ANAYFLXLLRPGSLRXCKXXQCFSXXARXIFKDXARTKLFWISY 45
    ||||| ||||| || ||||| ||||| ||||| ||||| |||||
Db  1 ANA-FLXLLRPGSLRXCKXXQCFSXXARXIFKDXARTKLFWISY 44
    ||||| ||||| || ||||| ||||| ||||| ||||| |||||

RESULT 4
ADD50096
ID  ADD50096 standard; protein; 44 AA.
XX
AC  ADD50096;
XX
DT  15-JAN-2004 (first entry)
XX
DE  Human vitamin K-dependent protein #2.
XX
```

KW Human; vitamin K-dependent protein; gamma-carboxyglutamic acid domain;
KW GLA domain; membrane binding affinity; clot formation; haemophilia;
KW clotting disorder; site directed mutagenesis; haemostatic; anticoagulant;
KW thrombolytic.
XX
XX Homo sapiens.
XX
XX US2003100506-A1.
XX
XX PD 29-MAY-2003.
XX
XX PF 18-NOV-2002; 2002US-00298330.
XX
XX PR 23-OCT-1997; 97US-00955636.
XX PR 29-APR-1999; 99US-00302239.
XX PR 03-FEB-2000; 2000US-00497591.
XX
XX PA (NELS/) NELSESTUEN G L.
XX
XX FI Nelsestuen GL;
XX
XX DR WPI; 2003-606646/57.
XX
XX PT New vitamin K-dependent polypeptide for modulating clot formation in
XX mammals comprises a modified gamma-carboxyglutamic acid domain that
XX enhances membrane binding affinity and activity of the polypeptide.
XX
XX PS Example 5; SEQ ID NO 3; 51pp; English.
XX
XX CC The invention relates to a vitamin K-dependent polypeptide comprising a
XX modified gamma-carboxyglutamic acid (GLA) domain that enhances membrane
XX binding affinity and activity of the polypeptide relative to a
XX corresponding native vitamin K-dependent polypeptide, where the modified
XX GLA domain comprises a glutamic acid residue at position 34. The
XX polypeptide is useful in modulating clot formation in mammals or in
XX treating certain types of haemophilia or clotting disorders. The membrane
XX binding affinity of polypeptides is increased by site directed
XX mutagenesis in the GLA domain. This sequence represents a vitamin K-
XX dependent protein of the invention.
XX
XX SQ Sequence 44 AA;
Query Match 81.2%; Score 161.5; DB 7; Length 44;
Best Local Similarity 97.8%; Pred. No. 7.2e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 ANAYFLXXLRPGSLXXRCXXQCSPXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLXXLRPGSLXXRCXXQCSPXXARXIFKDXRTKLFWISY 44
RESULT 5
ADQ26902
ID ADQ26902 standard; protein; 44 AA.
XX
XX AC ADQ26902;
XX
XX DT 26-AUG-2004 (first entry)
XX
XX DE Human factor VII gamma-carboxyglutamic acid (GLA) domain.
XX
XX KW Human; clot formation; protein C; activated protein C; APC;
KW gamma-carboxyglutamic acid domain; GLA domain; vitamin K-dependent;
KW aspirin; warfarin; heparin; haemophilic disorder; haemostatic;
KW anticoagulant; factor VII.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX Misc-difference 1: 44
XX /label= OTHER
XX /note= "OTHER= All Xaa residues are glutamic acid or
XX gamma carboxyglutamic acid"

XX US6747003-B1.
XX
XX PD 08-JUN-2004.
XX
XX PF 03-FEB-2000; 2000US-00497591.
XX
XX PR 23-OCT-1997; 97US-00955636.
XX PR 29-APR-1999; 99US-00302239.
XX
XX PA (MINU) UNIV MINNESOTA.
XX
XX FI Nelsestuen GL;
XX
XX DR WPI; 2004-429803/40.
XX
XX PT Decreasing clot formation by administering an anticoagulant agent, and a
XX protein C or activated protein C polypeptide having a modified GLA
XX domain, useful for treating hemophilic disorders in mammals.
XX
XX PS Example 5; SEQ ID NO 3; 41pp; English.
XX
XX CC The invention relates to a method of decreasing clot formation comprising
XX administering to a patient an anticoagulant agent and a protein C or
XX activated protein C (APC) polypeptide comprising a modified gamma-
XX carboxyglutamic acid (GLA) domain with two, three, four or five amino
XX acid substitutions. The invention also relates to vitamin K-dependent
XX nucleic acids, polypeptides, host cells, vectors and antibodies used in
XX the methods of the invention. The anticoagulant agent is aspirin,
XX warfarin or heparin, preferably aspirin. The methods and compositions of
XX the present invention are useful for modulating clot formation for
XX treating haemophilic disorders in mammals. This sequence represents the
XX human factor VII GLA domain, used in the method of the invention.
XX
XX SQ Sequence 44 AA;
Query Match 81.2%; Score 161.5; DB 8; Length 44;
Best Local Similarity 97.8%; Pred. No. 7.2e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 ANAYFLXXLRPGSLXXRCXXQCSPXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLXXLRPGSLXXRCXXQCSPXXARXIFKDXRTKLFWISY 44
RESULT 6
AAB84870
ID AAB84870 standard; protein; 401 AA.
XX
XX AC AAB84870;
XX
XX DT 31-JUL-2001 (first entry)
XX
XX DE Mutant blood coagulant factor VII (FVII-31).
XX
XX KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KW mutant; mutein.
XX
XX OS Homo sapiens.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX Misc-difference 311: 317
XX /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp -
XX Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
XX
XX PN JP2001061479-A.
XX
XX PD 13-MAR-2001.
XX
XX PF 24-AUG-1999; 99JP-00237610.
XX
XX PR 24-AUG-1999; 99JP-00237610.

XX PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
XX WPI; 2001-310677/33.
DR N-PSDB; AAH19463.
XX
XX Mutant of blood coagulant factor VII, used for substitution therapy in
PT the treatment of hemophilia.
XX
XX Claim 14; Page 20-21; 29pp; Japanese.
XX
XX The present invention relates to mutants of blood coagulant factor VII
CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
CC sequence is one such mutant FVII: VII-31. The mutants can be used as an
CC agent for the substitution therapy of haemophilia inhibitor patients
XX
XX Sequence 401 AA;
SQ
Query Match 81.2%; Score 161.5; DB 4; Length 401;
Best Local Similarity 75.6%; Pred. No. 6.9e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
QY 1 ANAYFLXXLRPGSLXRXCKXQCXFXXARXIFKDXRTKLFWISY 45
DB 1 ANA-FLLELRPGSLERECKEQCSFEAREIFKDAERTKLFWISY 44
RESULT 7
AAB84871
ID AAB84871 standard; protein; 401 AA.
XX
XX AAB84871;
XX
XX 31-JUL-2001 (first entry)
XX
XX Mutant blood coagulant factor VII (FVII-39).
XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
XX mutant; mutuin.
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 235..239
FT /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by Asp-
FT Arg-Lys-Thr-Leu"
FT Misc-difference 311..317
FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp -
FT Ser-Pro-Ana substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
XX JP2001061479-A.
XX
XX 13-MAR-2001.
XX
XX 24-AUG-1999; 99JP-00237610.
XX
XX 24-AUG-1999; 99JP-00237610.
XX
XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
XX WPI; 2001-310677/33.
DR N-PSDB; AAH19464.
XX
XX Mutant of blood coagulant factor VII, used for substitution therapy in
PT the treatment of hemophilia.
XX
XX Claim 16; Page 23-24; 29pp; Japanese.
XX
XX The present invention relates to mutants of blood coagulant factor VII
CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
CC sequence is one such mutant FVII: VII-39. The mutants can be used as an
CC agent for the substitution therapy of haemophilia inhibitor patients
XX

XX SQ Sequence 401 AA;
XX
XX Query Match 81.2%; Score 161.5; DB 4; Length 401;
Best Local Similarity 75.6%; Pred. No. 6.9e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
QY 1 ANAYFLXXLRPGSLXRXCKXQCXFXXARXIFKDXRTKLFWISY 45
DB 1 ANA-FLLELRPGSLERECKEQCSFEAREIFKDAERTKLFWISY 44
RESULT 8
AAR35764
ID AAR35764 standard; protein; 406 AA.
XX
XX AAR35764;
XX
XX 25-MAR-2003 (revised)
DT 24-SBP-1993 (first entry)
XX
XX Factor VII (VII).
XX PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;
XX Factor VII; CT; chymotrypsinogen; SP; serine protease; binding; exosite;
XX catalytic activity.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Region 1..152
FT /note= "Factor VII light chain"
FT Region 153..406
FT /note= "Factor VII heavy chain"
FT Peptide 245..266
FT /note= "Claim 9, page 138-139 describes an antibody that
FT reacts with Factor VII; fragments 289-304, 290-304, 290-
FT 310, 374-388 and 400-414 but not with fragment 245-266"
FT Peptide 289..304
FT /note= "pref. PC polypeptide; claim 4, page 137"
FT Peptide 290..310
FT /note= "exosite 2"
FT Peptide 290..310
FT /note= "pref. PC polypeptide; claim 2, page 136"
FT Peptide 290..304
FT /note= "pref. PC polypeptide; claim 4, page 137"
FT Peptide 374..388
FT /note= "exosite 1"
FT Peptide 374..388
FT /note= "pref. PC polypeptide; claim 2, page 136"
XX WO9309804-A1.
XX
XX 27-MAY-1993.
XX
XX 18-NOV-1992; 92WO-US010242.
XX
XX 18-NOV-1991; 91US-00793989.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Griffin JH, Mesters RM;
XX WPI; 1993-182244/22.
XX
XX Serine protease derived-polypeptide(s) and anti-peptide antibodies - for
PT inhibiting coagulation and assaying for the presence of serine protease
PT in fluid samples.
XX
XX Disclosure; Page 133-135; 149pp; English.
XX
XX The PC polypeptides indicated in the Features Table inhibit coagulation
CC (they prevent binding of serine protease to natural substrates), esp.
CC

CC when admin. to give an intravascular blood concn. of 0.1-100 (pref. 0.5-
CC 10) microm. NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are
CC described in the specification but have not yet been added to the
CC SEQUENCE LISTING. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 406 AA;

Query Match 81.2%; Score 161.5; DB 2; Length 406;
Best Local Similarity 75.6%; Pred. NO. 7e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAYELXXLRCSLXXCKXQCSPXXARXIFKDAERTKLFWISY 45
Db 1 ANA-FLERPGSLRECKEQCSPEAREIFKDAERTKLFWISY 44

RESULT 9
AAW14510
ID AAW14510 standard; protein; 406 AA.
XX
AC AAW14510;
XX
XX 25-MAR-2003 (revised)
DT 14-MAY-1997 (first entry)
XX
XX Modified blood coagulation Factor VII (R315S).
DE
XX
XX Blood coagulation; factor 7; mutein; mutation; modification;
KW thrombocytopenia; von Willebrand's disease; plasma substitute.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Modified-site 6
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 7
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 14
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 16
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 17
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Disulfide-bond 17. .22
FT Modified-site 19
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 20
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 25
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 26
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 29
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Cleavage-site 32. .33
FT /note= "proteolytic site"
FT Modified-site 35
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Cleavage-site 38. .39
FT /note= "proteolytic site"
FT Cleavage-site 42. .43
FT /note= "proteolytic site"
FT Cleavage-site 44. .45
FT /note= "proteolytic site"

FT Disulfide-bond 50. .61
FT Disulfide-bond 55. .70
FT Modified-site 63
FT /label= OTHER
FT /note= "beta-hydroxy-aspartic acid"
FT Disulfide-bond 72. .81
FT Disulfide-bond 91. .102
FT Disulfide-bond 98. .112
FT Disulfide-bond 114. .127
FT Disulfide-bond 135. .162
FT Cleavage-site 143. .144
FT /note= "proteolytic site"
FT Modified-site 145
FT /note= "glycosylation site"
FT Disulfide-bond 159. .164
FT Disulfide-bond 178. .194
FT Active-site 193
FT Active-site 242
FT Cleavage-site 290. .291
FT /note= "proteolytic site"
FT Disulfide-bond 310. .329
FT Cleavage-site 315. .316
FT /note= "proteolytic site in unmodified factor VII"
FT Misc-difference 315
FT /note= "native Arg315 has been substituted by Ser to
FT provide a proteolytically more stable peptide bond"
FT Modified-site 322
FT /note= "glycosylation site"
FT Disulfide-bond 340. .368
FT Cleavage-site 341. .342
FT /note= "proteolytic site"
FT Active-site 344
FT Cleavage-site 392. .393
FT /note= "proteolytic site"
FT Cleavage-site 396. .397
FT /note= "proteolytic site"
FT Cleavage-site 402. .403
FT /note= "proteolytic site"
XX US5580560-A.
XX
XX 03-DEC-1996.
XX
XX 22-AUG-1994; 94US-00293778.
XX
XX 13-NOV-1989; 89US-00434149.
XX 12-JUN-1992; 92US-00898248.
XX 09-AUG-1993; 93US-00104509.
XX
XX (NOVO) NOVO-NORDISK AS.
XX
XX Wiberg FC, Woodbury R, Nicolaisen EM, Bjorn SE;
XX WPI; 1997-033523/03.
XX
XX Mutated human factor VII or VIIa proteins - with amino acid substitutions
XX to improve proteolytic stability.
XX
XX Example 4; Page; 28pp; English.
XX
XX Modified human factor VII or VIIa proteins are stabilised against
XX proteolytic cleavage by substitution of one of the residues Lys32, Lys38,
XX Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and Lys341 by an
XX amino acid that provides a proteolytically more stable peptide bond,
XX provided that Lys32 is replaced by Gln, Glu, His, Gly, Thr, Ala or Ser.
XX The modified proteins are useful for treating bleeding disorders such as
XX thrombocytopenia and von Willebrand's disease. They are also suitable for
XX addition to plasma substitutes. The present sequence is a specific
XX example of a modified factor VII protein. (Updated on 25-MAR-2003 to
XX correct PP field.)
SQ Sequence 406 AA;


```

RESULT 12
AAB84867
ID AAB84867 standard; protein; 406 AA.
XX
XX AAB84867;
XX
XX 31-JUL-2001 (first entry)
XX
XX Mutant blood coagulant factor VII (FVII-5).
DE
DE Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KW mutant; muten.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 159
FT /note= "Wild-type Cys substituted by Ala"
FT Misc-difference 164
FT /note= "Wild-type Cys substituted by Ala"
XX
XX JP2001061479-A.
XX
XX 13-MAR-2001.
XX
XX 24-AUG-1999; 99JP-00237610.
XX
XX 24-AUG-1999; 99JP-00237610.
XX
XX (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
XX WPI; 2001-310677/33.
DR N-PSDB; AAH19460.
XX
XX
XX Mutant of blood coagulant factor VII, used for substitution therapy in
the treatment of hemophilia.
XX
XX Claim 3; Page 11-12; 29pp; Japanese.
XX
XX The present invention relates to mutants of blood coagulant factor VII
(FVII) or activated blood coagulant factor VII (FVIIa). The present
sequence is one such mutant FVII: VII-5. In the wild-type protein
(AAB84866), there is a disulphide bond (159Cys-164Cys). In the present
protein, the disulphide bond is disrupted. The mutants can be used as an
agent for the substitution therapy of haemophilia inhibitor patients
XX
XX Sequence 406 AA;
SQ
Query Match 81.2%; Score 161.5; DB 4; Length 406;
Best Local Similarity 75.6%; Pred. No. 7e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps
QY 1 ANAYFLXLRPGSLRXKCKXXQCQFXXARXIFKDAXRTKLEWISY 45
| | | | | | | | | | | | | | | | | | | | | |
DB 1 ANA-FLESLRPGSLRECKEESQCFEAREIFKDAERTKLEWISY 44
| | | | | | | | | | | | | | | | | | | | | |

RESULT 13
AAB84868
ID AAB84868 standard; protein; 406 AA.
XX
XX AAB84868;
XX
XX 31-JUL-2001 (first entry)
XX
XX Mutant blood coagulant factor VII (FVII-6).
DE
DE Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KW mutant; muten.
XX
XX Homo sapiens.
OS

```

OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 164
 FT /note= "Wild-type Cys substituted by Ala"
 FT Misc-difference 299
 FT /note= "Wild-type Val substituted by Cys"
 XX
 XX JP2001061479-A.
 XX
 XX 13-MAR-2001.
 XX
 XX 24-AUG-1999; 99JP-00237610.
 XX
 XX 24-AUG-1999; 99JP-00237610.
 XX
 XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX
 XX WPI; 2001-310677/33.
 DR N-PSDB; AAH19461.
 XX
 XX Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia.
 XX
 XX Claim 5; Page 14-15; 29pp; Japanese.
 XX
 XX The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-6. In the wild-type protein
 CC (AAB84866), there is a disulphide bond (159Cys-164Cys). In the present
 CC protein, the disulphide bond is disrupted. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients
 XX
 XX Sequence 406 AA;
 SQ
 Query Match 81.2%; Score 161.5; DB 4; Length 406;
 Best Local Similarity 75.6%; Pred. No. 7e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
 Qy 1 ANAYFLXXLRPGSLRXKCKXXQCQSFXXARXIFKDAERTKLFWISY 45
 Db 1 ANA-FLEELRPGSLERECKEQCSFEAREIFKDAERTKLFWISY 44
 RESULT 14
 AAB84869
 ID AAB84869 standard; protein; 406 AA.
 AC AAB84869;
 XX
 XX 31-JUL-2001 (first entry)
 XX
 XX Mutant blood coagulant factor VII (FVII-30).
 DE Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 KW mutant; mutein.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 235..239
 FT /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by Asp-
 FT Arg-Lys-Thr-Leu"
 XX
 XX JP2001061479-A.
 XX
 XX 13-MAR-2001.
 XX
 XX 24-AUG-1999; 99JP-00237610.
 XX
 XX 24-AUG-1999; 99JP-00237610.

PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX
 XX WPI; 2001-310677/33.
 DR N-PSDB; AAH19462.
 XX
 XX Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia.
 XX
 XX Claim 9; Page 17-18; 29pp; Japanese.
 XX
 XX The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-30. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients
 XX
 XX Sequence 406 AA;
 SQ
 Query Match 81.2%; Score 161.5; DB 4; Length 406;
 Best Local Similarity 75.6%; Pred. No. 7e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
 Qy 1 ANAYFLXXLRPGSLRXKCKXXQCQSFXXARXIFKDAERTKLFWISY 45
 Db 1 ANA-FLEELRPGSLERECKEQCSFEAREIFKDAERTKLFWISY 44
 RESULT 15
 AAB84866
 ID AAB84866 standard; protein; 406 AA.
 XX
 XX AAB84866;
 AC
 XX
 XX 31-JUL-2001 (first entry)
 XX
 XX Wild-type human blood coagulant factor VII (FVII).
 DE Human; haemostatic; blood coagulant factor VII; FVII; haemophilia.
 KW Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 159..164
 FT
 XX JP2001061479-A.
 XX
 XX 13-MAR-2001.
 XX
 XX 24-AUG-1999; 99JP-00237610.
 XX
 XX 24-AUG-1999; 99JP-00237610.
 XX
 XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX
 XX WPI; 2001-310677/33.
 DR N-PSDB; AAH19459.
 XX
 XX Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia.
 XX
 XX Disclosure; Page 8-9; 29pp; Japanese.
 XX
 XX The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence represents the protein sequence for wild-type human FVII. The
 CC mutants can be used as an agent for the substitution therapy of
 CC haemophilia inhibitor patients
 XX
 XX Sequence 406 AA;
 SQ
 Query Match 81.2%; Score 161.5; DB 4; Length 406;
 Best Local Similarity 75.6%; Pred. No. 7e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAVFLXXLRPGSLRXCKXOCSPXXARXIFKDAERTKLFWISY 45
Db 1 ANA-FLEELRPGSLERECKEEOCSFEAREIFKDAERTKLFWISY 44

Search completed: August 22, 2005, 18:45:41
Job time : 93 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2005, 09:28:04 ; Search time 25 Seconds
(without alignments)
173.190 Million cell updates/sec

Title: US10031005-3Y4
Perfect score: 199
Sequence: 1 ANAYFLXXLRPGSLRXCKX.....XXARXIFDXARTKLFWISY 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	161.5	81.2	466	1 KFHU7	coagulation factor
2	127.5	64.1	443	2 I46932	coagulation factor
3	113	56.8	407	1 KFO7	coagulation factor
4	98.5	49.5	461	1 JX0210	protein C (activat
5	93.5	47.0	456	1 KXBO	protein C (activat
6	91.5	46.0	488	1 EXHU	coagulation factor
7	90.5	45.5	492	1 EXBO	coagulation factor
8	89.5	45.0	461	1 S18994	protein C (activat
9	88.5	44.5	482	1 EXRT	coagulation factor
10	86	43.2	416	1 KFO	coagulation factor
11	86	43.2	617	2 S10511	thrombin (EC 3.4.2
12	86	43.2	618	2 A35827	thrombin (EC 3.4.2
13	83	41.7	461	1 KFHU	coagulation factor
14	80.5	40.5	475	1 EXCH	coagulation factor
15	78	39.2	452	1 A30351	coagulation factor
16	78	39.2	459	2 JQ0419	coagulation factor
17	75	37.7	396	1 KXBOZ	plasma protein 2 -
18	73.5	36.9	461	1 KKHU	protein C (activat
19	73	36.7	622	1 TBHU	thrombin (EC 3.4.2
20	70	35.2	422	1 KKHUZ	plasma protein 2 p
21	69	34.7	625	1 TBBO	thrombin (EC 3.4.2
22	61.5	30.9	576	2 G36763	probable MAP kinas
23	61	30.7	594	2 D84859	probable MAP kinas
24	61	30.7	603	2 G36575	probable MAP kinas
25	58.5	29.4	642	2 S53433	plasma protein S p
26	56	28.1	675	1 KXBOS	plasma protein S p
27	55.5	27.9	675	1 KXMS	plasma protein S p
28	55	27.6	673	2 A48089	growth arrest-spec
29	53.5	26.9	642	2 S53434	plasma protein S p

30 53.5 26.9 646 2 S38819 plasma protein S -
31 53.5 26.9 676 1 KXHUS plasma protein S p
32 53 26.6 674 2 I55476 growth potentiatin
33 53 26.6 675 1 KXRTS plasma protein S p
34 53 26.6 678 2 B48089 growth arrest-spec
35 47.5 23.9 319 2 T15137 hypothetical prote
36 46.5 23.4 516 2 H84424 probable MAP kinas
37 46 23.1 514 2 C64154 hypothetical prote
38 46 23.1 543 2 H84724 probable ARI-like
39 45 22.6 879 2 S55864 hypothetical prote
40 44 22.1 226 2 G96531 hypothetical prote
41 43.5 21.9 367 2 B56598 hypothelial kinase
42 43.5 21.9 385 2 T15221 hypothetical prote
43 43.5 21.9 1298 2 A48999 protein-tyrosine k
44 43.5 21.9 1363 2 I58375 protein-tyrosine k
45 43.5 21.9 1379 2 JC4954 vascular endotheli

RESULT 1
KFHU7
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1989 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
C:Accession: A28322; A23819; A31186; B31186; S63524
R:O'Hara, P. J.; Grant, F. J.; Haldeman, B. A.; Gray, C. L.; Insley, M. Y.; Hagen, F. S.; Murze
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A:Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depende
A:Reference number: A28322; MUID:87260948; PMID:3037537
A:Accession: A28322
A:Molecule type: DNA
A:Residues: 1-466 <OHA>
A:Cross-references: UNIPROT:P08709; GB:J02933; NID:gl80333; PIDN:AAA51983.1; PID:gl80334
R:Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C.
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A:Title: Characterization of a cDNA coding for human factor VII.
A:Reference number: A23819; MUID:86205965; PMID:3486420
A:Accession: A23819
A:Molecule type: mRNA
A:Residues: 1-466 <HAG>
A:Cross-references: GB:M13232; NID:gl82799; PIDN:AAA88040.1; PID:gl82801
R:Thim, L.; Bjoern, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.F
Biochemistry 27, 7785-7793, 1988
A:Title: Amino acid sequence and posttranslational modifications of human factor VII-a f
A:Reference number: A90539; MUID:89088153; PMID:3264725
A:Accession: A31186
A:Molecule type: protein
A:Residues: 61-212 <THI>
A:Accession: B31186
A:Molecule type: protein
A:Residues: 213-466 <TH2>
R:Bjoern, S.; Foster, D.C.; Thim, L.; Wiberg, F.C.; Christensen, M.; Komiyama, Y.; Peders
J. Biol. Chem. 266, 11051-11057, 1991
A:Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations at
A:Reference number: A40529; MUID:91250411; PMID:1904059
A:Contents: annotation; carbohydrate binding sites
R:Persson, E.; Petersen, L.C.
Eur. J. Biochem. 234, 293-300, 1995
A:Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carboxy
A:Reference number: S63524; MUID:96096752; PMID:8529655
A:Accession: S63524
A:Molecule type: protein
A:Residues: 61-65;99-103,105-109;213-217;308-312 <PER>
C:Genetics:
A:Gene: GDB:F7
A:Cross-references: GDB:119897; OMIM:227500
A:Map position: 13q34-13q34
A:Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the preser
coagulation factor IX in the presence of calcium and tissue factor

ALIGNMENTS

A;Pathway: blood coagulation extrinsic pathway
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-60/Domain: propeptide #status predicted <PRO>
F;45-104/Domain: Gla domain homology <GLA>
F;61-212/Product: coagulation factor VIIa light chain #status experimental <MA1>
F;110-141/Domain: EGF homology <EG1>
F;151-187/Domain: EGF homology <EG2>
F;213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F;213-447/Domain: trypsin homology <TRY>
F;66,67,74,76,79,80,85,86,89,95/Modified site: gamma-carboxyglutamic acid (Glu) #status
F;77-82,110-121,115-130,132-141,158-162,158-172,174-187,195-322,219-224,238-254,370-389,
F;112,120/Binding site: carboxyhydrate (Ser) (covalent) #status experimental
F;123/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent
F;205,382/Binding site: carboxyhydrate (Asn) (covalent) #status experimental
F;212-213/Cleavage site: Arg-Ile (coagulation factor XIIa) #status experimental
F;253,302,404/Active site: His, Asp, Ser #status predicted
F;350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted

Query Match 81.2%; Score 161.5; DB 1; Length 466;
Best Local Similarity 75.6%; Pred. No. 2.5e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLRXKCKXXQCXFXRXARXIFKDXRTKLFWSY 45
Db 61 ANA-FLEELRPGSLERECKEQCSFEAREIFKDAERTKLFWSY 104

RESULT 2
146932
coagulation factor VII - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
C;Accession: I46932
R;Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
Thromb. Res. 69, 231-238, 1993
A;Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
A;Reference number: I46932; MUID:93190306; PMID:838365
A;Accession: I46932
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-443 <BRO>
A;Cross-references: GB:S56300; NID:g266294; PID:g266295
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology <GLA>
F;89-120/Domain: EGF homology <EG1>
F;130-166/Domain: EGF homology <EG2>
F;192-425/Domain: trypsin homology <TRY>

Query Match 64.1%; Score 127.5; DB 2; Length 443;
Best Local Similarity 57.8%; Pred. No. 1.4e-13;
Matches 26; Conservative 4; Mismatches 14; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLRXKCKXXQCXFXRXARXIFKDXRTKLFWSY 45
Db 40 ANS-FLEELRPGSLERECKEQCSFEAREVFQSTERTKQFWY 83

RESULT 3
KF07
coagulation factor VIIa (EC 3.4.21.21) - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: A31979; C20274
R;Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.
J. Biol. Chem. 263, 14868-14877, 1988
A;Title: Bovine factor VII. Its purification and complete amino acid sequence.
A;Reference number: A31979; MUID:89008362; PMID:3049594
A;Accession: A31979
A;Molecule type: protein
A;Residues: 1-407 <TAK>
A;Cross-references: UNIPROT:P22457

R;McMullen, B.A.; Fujikawa, K.; Kiesel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor VII.
A;Reference number: A20274; MUID:83308813; PMID:6688526
A;Accession: C20274
A;Molecule type: protein
A;Residues: 58-62, 'X', 64-68 <MCM>
A;Note: the residue designated 'X' was determined to be hydroxyaspartic acid
R;Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, S.
J. Biochem. 104, 867-868, 1988
A;Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factor VII.
A;Reference number: A45556; MUID:89213999; PMID:3149637
A;Contents: annotation
A;Note: structure and location of covalently bound carbohydrate
C;Function:
A;Description: catalyzes the proteolytic activation of coagulation factor X in the presence of calcium and tissue factor
A;Pathway: blood coagulation extrinsic pathway
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
F;1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>
F;1-44/Domain: Gla domain homology (fragment) <GLA>
F;50-81/Domain: EGF homology <EG1>
F;91-127/Domain: EGF homology <EG2>
F;153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F;153-387/Domain: trypsin homology <TRY>
F;6,7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #status
F;17-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-368/I
F;52/Binding site: carboxyhydrate (Ser) (covalent) #status experimental
F;63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experimental
F;145-203/Binding site: carboxyhydrate (Asn) (covalent) #status experimental
F;152-153/Cleavage site: Arg-Ile (coagulation factor XIIa) #status experimental
F;193,242,344/Active site: His, Asp, Ser #status predicted
F;290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match 56.8%; Score 113; DB 1; Length 407;
Best Local Similarity 51.2%; Pred. No. 3.6e-11;
Matches 21; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 5 FLXXLRPGSLRXKCKXXQCXFXRXARXIFKDXRTKLFWSY 45
Db 4 FLEELRPGSLERECKEQCSFEAREVFQSTERTKQFWY 44

RESULT 4
JX0210
protein C (activated) (EC 3.4.21.69) precursor - mouse
N;Alternate names: vitamin K-dependent serine proteinase
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JX0210
R;Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
J. Biochem. 111, 491-495, 1992
A;Title: Isolation and characterization of a mouse protein C cDNA.
A;Reference number: JX0210; MUID:92316897; PMID:1618739
A;Accession: JX0210
A;Molecule type: mRNA
A;Residues: 1-461 <TAD>
A;Cross-references: UNIPROT:P33587; GB:D10445; NID:g220385; PID:BAA01235.1; PID:g220386
A;Experimental source: liver
C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that regulates blood coagulation.

C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
F;1-33/Domain: signal sequence #status predicted <SIG>
F;27-83/Domain: Gla domain homology <GLA>
F;34-41/Domain: propeptide #status predicted <PRO>
F;42-196,199-461/Product: protein C #status predicted <PC>
F;42-196/Domain: light chain #status predicted <PCL>
F;91-130/Domain: EGF homology <EG1>
F;139-174/Domain: EGF homology <EG2>
F;199-461/Domain: heavy chain #status predicted <PCH>
F;199-211/Domain: activation peptide #status predicted <ACT>

A;Title: Characterization of a cDNA coding for human factor X.
A;Reference number: A21284; MUID:84222026; PMID:6587384
A;Accession: A21284
A;Molecule type: mRNA
A;Residues: 13-284, 'E', 289-488 <LE2>
A;Cross-references: GB:K01886
R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weine Biochemistry 22, 2875-2884, 1983
A;Title: Complete amino acid sequence of the light chain of human blood coagulation factor X.
A;Reference number: A20362; MUID:83257207; PMID:6871167
A;Accession: A20362
A;Molecule type: protein
A;Residues: 41-179 <MCM>
R;Inoue, K.; Morita, T.
Eur. J. Biochem. 218, 153-163, 1993
A;Title: Identification of O-linked oligosaccharide chains in the activation peptides of factor X.
A;Reference number: S39414; MUID:94062825; PMID:8243461
A;Accession: S39415
A;Molecule type: protein
A;Residues: 183-234 <INO>
A;Note: Glycosylation sites
A;Note: Identification and characterization of beta-hydroxyaspartic acid
R;Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhusanam, K.; Lyman, G. Gene 84, 517-519, 1989
A;Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human factor X.
A;Reference number: 154051; MUID:90128299; PMID:2612918
A;Accession: 154051
A;Status: translation not shown; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-23 <RES>
A;Cross-references: GB:M33287; NID:G183860; PIDN:AAA52636.1; PID:G553330
R;Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Blass J. Mol. Biol. 232, 947-966, 1993
A;Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
A;Reference number: A49458; MUID:93360277; PMID:8355279
A;Contents: annotation; X-ray crystallography, 2.2 angstroms
C;Comment: The two chains held together by one disulfide bond are formed from a single-cysteine chain.
C;Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or factor XIa.
C;Genetics:
A;Gene: GDB:F10
A;Cross-references: GDB:119890; OMIM:227600
A;Map position: 13q34-13q34
A;Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
A;Note: deficiency of this factor causes Stuart disease
C;Function:
A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of factor V.
A;Pathway: blood coagulation
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-40/Domain: propeptide #status predicted <PRO>
F;25-84/Domain: Gla domain homology <GLA>
F;41-179/Product: coagulation factor X light chain #status experimental <LCH>
F;90-121/Domain: EGF homology <EGF>
F;129-164/Domain: EGF homology <EGF>
F;183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
F;235-488/Product: coagulation factor X heavy chain #status experimental <ACT>
F;235-462/Domain: trypsin homology <TRY>
F;46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted
F;57-62/Disulfide bonds: #status predicted
F;90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F;199,211/Binding site: carboxyglutamate (Thr) (covalent) #status experimental
F;221,231/Binding site: carboxyglutamate (Asn) (covalent) #status experimental
F;234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #status predicted
F;276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 46.0%; Score 91.5; DB 1; Length 488;
Best Local Similarity 40.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 8; Mismatches 18; Indels 1; Gaps 1;
Qy 1 ANAYFLXLRPGSLRXKCKXQCFFXXARXIFDKAXTKLFWISY 45

Db 41 ANS-FLEEMKKGHLERCMBETCSYBEAREVFDSDKTNFWMKY 84
RESULT 7
EXBO
coagulation factor Xa (BC 3.4.21.6) precursor - bovine
N;Alternate names: Stuart factor
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Apr-1984 #sequence revision 17-Mar-1987 #text change 09-Jul-2004
C;Accession: A22867; A14997; A12030; A34412; S39414; A00925
R;Fung, M.R.; Campbell, R.M.; MacGillivray, T.A.
Nucleic Acids Res. 12, 4481-4492, 1984
A;Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a signal peptide.
A;Reference number: A22867; MUID:84247315; PMID:6330671
A;Accession: A22867
A;Molecule type: mRNA
A;Residues: 1-487 <FUN>
A;Cross-references: UNIPROT:P00743; GB:X00673; NID:G192; PIDN:CAA25286.1; PID:G193
R;Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K. Biochemistry 19, 659-667, 1980
A;Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
A;Reference number: A14997; MUID:80130563; PMID:6766735
A;Accession: A14997
A;Molecule type: protein
A;Residues: 41-102, 'N', 104-180 <ENF>
R;McMullen, B.A.; Fujikawa, K.; Kisiel, W. Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factors.
A;Reference number: A20274; MUID:83308813; PMID:6688526
R;Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H. Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
A;Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
A;Reference number: A12030; MUID:76053069; PMID:1059093
A;Accession: A12030
A;Molecule type: protein
A;Residues: 183-292,294-295, 'GDE',299-334,336-348, 'AE',351-354,356-441, 'GRFG',446-492 <TJ>
A;Note: carboxylate binding sites and disulfide bonds were determined
R;Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J. J. Biol. Chem. 264, 16897-16904, 1989
A;Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal factor X.
A;Reference number: A34412; MUID:89380326; PMID:2789221
A;Accession: A34412
A;Molecule type: protein
A;Residues: 85-126 <PER>
A;Note: beta-hydroxyaspartic acid site
R;Inoue, K.; Morita, T. Eur. J. Biochem. 218, 153-163, 1993
A;Title: Identification of O-linked oligosaccharide chains in the activation peptides of factor X.
A;Reference number: S39414; MUID:94062825; PMID:8243461
A;Accession: S39414
A;Molecule type: protein
A;Residues: 183-196,199-209,216-233 <INO>
A;Note: carboxylate binding sites
R;Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; DeWitt, D.L. Biochemistry 11, 4899-4903, 1972
A;Title: Bovine factor X-la (activated Stuart factor). Evidence of homology with mammalian factor X.
A;Reference number: A12453; MUID:73053314; PMID:4264286
A;Contents: annotation; active site
R;Fujikawa, K.; Titani, K.; Davie, E.W. Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
A;Title: Activation of bovine factor X (Stuart factor): conversion of factor Xa to factor Xa1.
A;Reference number: A13504; MUID:76053121; PMID:1059122
A;Contents: annotation; activation
R;Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J. J. Biol. Chem. 259, 5705-5710, 1984
A;Title: Calcium-binding properties of bovine factor X (Stuart factor).
A;Reference number: A38024; MUID:84185716; PMID:6546930
A;Contents: annotation; calcium binding
R;Morita, T.; Jackson, C.W. J. Biol. Chem. 261, 4008-4014, 1986
A;Reference number: A38025; MUID:86140210; PMID:3949800

A:Contents: annotation; sulfate binding
 C:Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
 C:Comment: The two chains are formed from a single-chain precursor by the excision of two chains.
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), and activation.
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strong C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin C:Genetics:
 A:Gene: F10
 A:Map position: 13q34
 C:Function:
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of calcium
 A:Pathway: blood coagulation
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic acid
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-40/Domain: propeptide #status predicted <PRO>
 F:234-461/Domain: trypsin homology <TRY>
 F:46-47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted
 F:57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-341/Disulfide bonds: #status predicted
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:200/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
 F:208,485/Binding site: carboxylate (Thr) (covalent) #status experimental
 F:218/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:233-234/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #status predicted
 F:240-245,260-276,389-403,414-442/Disulfide bonds: #status experimental
 F:275,321,418/Active site: His, Asp, Ser #status predicted

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 Best Local Similarity 42.2%; Pred. No. 2.8e-07;
 Matches 19; Conservative 7; Mismatches 18; Indels 1; Gaps 1;

Qy 1 ANAYFLXLRPGSLXRCXKXQCXFXARXIFKDXARXKLFWISY 45
 Db 41 ANS-FLEVRKQGNLERECLEACSLSEAREVFEDAEQDFWISKY 84

RESULT 8
 S18994
 Protein C (activated) (EC 3.4.21.69) precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: S18994; S24312
 R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
 submitted to the EMBL Data Library, February 1992
 A:Description: The cDNA cloning and mRNA expression of rat protein C.
 A:Reference number: S18994
 A:Accession: S18994
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-461 <OKA>
 A:Cross-references: UNIPROT:P31394; EMBL:X64336; PIDN:CAA45617.1; PID:g56963
 R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
 Biochim. Biophys. Acta 1131, 329-332, 1992
 A:Title: The cDNA cloning and mRNA expression of rat protein C.
 A:Reference number: S24312; MUID:92329550; PMID:1627650
 A:Accession: S24312
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-461 <OKA2>
 A:Cross-references: EMBL:X64336; PIDN:CAA45617.1; PID:g56963
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase
 F:1-32/Domain: signal sequence #status predicted <SIG>
 F:27-85/Domain: Gla domain homology <GLA>
 F:33-42/Domain: propeptide #status predicted <PRO>

F:43-461/Product: protein C #status predicted <PRC>
 F:91-130/Domain: EGF homology <EG2>
 F:139-174/Domain: EGF homology <EG2>
 F:213-445/Domain: trypsin homology <TRY>
 F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted
 F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F:121-130,139-150,146-159,161-174,182-320,239-255,373-387,398-426/Disulfide bonds: #status predicted
 F:215,291,355/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:254,300,402/Active site: His, Asp, Ser #status predicted

Query Match 45.0%; Score 89.5; DB 1; Length 461;
 Best Local Similarity 44.4%; Pred. No. 3.9e-07;
 Matches 20; Conservative 5; Mismatches 19; Indels 1; Gaps 1;

Qy 1 ANAYFLXLRPGSLXRCXKXQCXFXARXIFKDXARXKLFWISY 45
 Db 42 ANS-FLEVRKQGNLERECMEICDFEERQIFQNVEDTLAPWIKY 85

RESULT 9
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 coagulation factor Xa (EC 3.4.21.6) precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004
 C:Accession: S49075; JC4670; PS0191; PS0190; I62745
 R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
 Thromb. Res. 80, 63-73, 1995
 A:Title: Evidence for competition between vitamin K-dependent clotting factors for intracellular
 A:Reference number: A58498; MUID:96093366; PMID:8578539
 A:Accession: S49075
 A:Molecule type: mRNA
 A:Residues: 1-482 <STAL>
 A:Cross-references: UNIPROT:Q63207; EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g50661
 A:Note: submitted to the EMBL Data Library, June 1994
 A:Note: neither the complete nucleic acid sequence nor the complete translation are shown
 R:Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
 Gene 169, 269-273, 1996
 A:Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
 A:Reference number: JC4670; MUID:96194815; PMID:8647460
 A:Accession: JC4670
 A:Molecule type: mRNA
 A:Residues: 1-482 <STA2>
 A:Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601
 A:Experimental source: Cos-1 cell
 R:Enryoji, K.; Miyazaki, K.; Kato, H.
 J. Biochem. 109, 890-898, 1991
 A:Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plasma
 A:Reference number: PS0190; MUID:92041742; PMID:1718949
 A:Accession: PS0191
 A:Molecule type: protein
 A:Residues: 41-58,'X',60-65 <ENJ1>
 A:Accession: PS0190
 A:Molecule type: protein
 A:Residues: 183-186,'X',188-207 <ENJ2>
 R:Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
 Eur. J. Haematol. 52, 162-168, 1994
 A:Title: Analysis of the partial nucleotide sequences and deduced primary structures of factor X
 A:Reference number: I46196; MUID:94222160; PMID:8168596
 A:Accession: I62745
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 295-383,'G',385-455 <MUR>
 A:Cross-references: GB:D21215; NID:g415309; PIDN:BAA04756.1; PID:g455396
 C:Function:
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of calcium
 A:Pathway: blood coagulation
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic acid
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-40/Domain: propeptide #status predicted <PRO>
 F:25-84/Domain: Gla domain homology <GLA>
 F:41-179/Product: coagulation factor X light chain #status predicted <LCH>
 F:90-121/Domain: EGF homology <EG1>

Search completed: August 22, 2005, 18:46:43
Job time : 26 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2005, 09:28:04 ; Search time 83 Seconds
(without alignments)
277.633 Million cell updates/sec

Title: US10031005-3y4

Perfect score: 199

Sequence: 1 ANAYFLXLRPGSLRXCKX.....XXARXIFDAXRTKLFWISY 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	161.5	81.2	466 1 FA7_HUMAN	P08709 homo sapien
2	161.5	81.2	679 2 Q96PQ8	Q96PQ8 homo sapien
3	127.5	64.1	444 1 FA7_RABIT	P98139 oryctolagus
4	116.5	58.5	446 1 FA7_MOUSE	P70375 mus musculus
5	113	56.8	407 1 FA7_BOVIN	P22457 bos taurus
6	109	54.8	443 2 Q80HC9	Q80HC9 brachydanio
7	103.5	52.0	459 1 PRTC_FIG	Q96IP2 sus scrofa
8	98.5	49.5	460 1 PRTC_MOUSE	P33587 mus musculus
9	96	48.2	179 2 Q8TAS3	Q8TAS3 homo sapien
10	96	48.2	198 1 TMG2_MOUSE	Q8T182 mus musculus
11	96	48.2	202 1 TMG2_HUMAN	O14669 homo sapien
12	95	47.7	216 2 Q8DIH4	Q64IH4 xenopus tro
13	94	47.2	442 2 Q804X1	Q804X1 figu rubrip
14	93.5	47.0	425 2 Q804X7	Q804X7 gallus gall
15	93.5	47.0	446 1 FA7_RAT	Q8K3U6 rattus norv
16	93.5	47.0	456 1 PRTC_BOVIN	P00745 bos taurus
17	92	46.2	208 2 Q6GPL7	Q6GPL7 xenopus lae
18	92	46.2	537 2 Q804W8	Q804W8 figu rubrip
19	91.5	46.0	218 1 TMG1_HUMAN	O14668 homo sapien
20	91.5	46.0	266 2 Q8NEK6	Q8NEK6 homo sapien
21	91.5	46.0	488 1 FA10_HUMAN	P00742 homo sapien
22	90.5	45.5	492 1 FA10_BOVIN	P00743 bos taurus
23	89.5	45.0	461 1 PRTC_RAT	P31394 rattus norv
24	88.5	45.0	461 2 Q68FY8	Q68FY8 rattus norv
25	88.5	44.5	433 2 Q804X5	Q804X5 gallus gall
26	88.5	44.5	469 2 Q9GMD9	Q9GMD9 ornithorhyn
27	88.5	44.5	482 1 FA10_RAT	Q63207 rattus norv
28	88	44.2	471 2 Q804X6	Q804X6 gallus gall
29	87.5	44.0	490 1 FA10_RABIT	O19045 oryctolagus
30	87	43.7	226 1 TMG4_HUMAN	Q9BZD6 homo sapien
31	86.5	43.5	340 2 Q80Y26	Q80Y26 mus musculus

32	86.5	43.5	376 1 FA10_TROCA	P81428 tropidechia
33	86.5	43.5	432 2 Q6GNA2	Q89a2 xenopus lae
34	86.5	43.5	481 1 FA10_MOUSE	Q88947 mus musculus
35	86	43.2	49 2 Q95ME8	Q95ME8 bos taurus
36	86	43.2	416 1 FA9_BOVIN	P00741 bos taurus
37	86	43.2	617 1 THR8_RAT	P18292 rattus norv
38	86	43.2	618 1 THR8_MOUSE	P19221 mus musculus
39	85.5	43.0	524 2 Q7SXH8	Q7SXH8 brachydanio
40	85	42.7	434 2 Q7T3B6	Q7C3B6 brachydanio
41	84.5	42.5	376 1 FA10_HOPST	P83370 hoplocephal
42	83.5	42.0	458 1 PRTC_RABIT	Q28661 oryctolagus
43	83.5	42.0	462 2 Q6PAG2	Q6PAG2 xenopus lae
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45	83	41.7	461 1 FA9_HUMAN	P00740 homo sapien

ALIGNMENTS

RESULT 1
ID FA7_HUMAN
AC P08709; Q14339;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator) (SPCA) (Proconvertin) (Eptacog alfa).
GN Name=F7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86205965; PubMed=3486420;
RA Hagen F.S., Gray C.B., O'Hara P.J., Grant F.J., Saari G.C., Woodbury R.G., Hart C.B., Insley M.Y., Kiesel W., Kurachi K., Davie E.W.;
RT "Characterization of a cDNA coding for human factor VII.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260948; PubMed=3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y., Hagen F.S., Murray M.J.;
RT "Nucleotide sequence of the gene coding for human factor VII, a vitamin K-dependent protein participating in blood coagulation.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.
RA Rieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RT "SeattleSNPs: NHLBI H66682 program for genomic applications, UW-FHRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=89088153; PubMed=3264725;
RA Thim L., Bjorn S., Christensen M., Nicolaisen E.M., Lund-Hansen T., Pedersen A.H., Hedner U.;
RT "Amino acid sequence and posttranslational modifications of human factor VIIa from plasma and transfected baby hamster kidney cells.";
RL Biochemistry 27:7785-7793(1988).
RN [5]
RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RX MEDLINE=91250411; PubMed=1904059;
RA Bjorn S., Foster D.C., Thim L., Wiberg F.C., Christensen M., Komiyama Y., Pedersen A.H., Kiesel W.;
RT "Human plasma and recombinant factor VII. Characterization of O-glycosylations at serine residues 52 and 60 and effects of site-directed mutagenesis of serine 52 to alanine.";

RL J. Biol. Chem. 266:11051-11057(1991).
 RN [6]
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.
 RX MEDLINE=90062160; PubMed=2511201;
 RA Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T., Takao T.,
 RA Shimomura Y., Iwanaga S.;
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide (Xyl2-
 RT Glc) O-glycosidically linked to a serine residue in the first
 RT epidermal growth factor-like domain of human factors VII and IX and
 RT protein Z and bovine protein Z.";
 RL J. Biol. Chem. 264:20320-20325(1989).
 RN [7]
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.
 RX MEDLINE=91344709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
 RT "A new trisaccharide sugar chain linked to a serine residue in the
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";
 RL Adv. Exp. Med. Biol. 281:121-131(1990).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=96175641; PubMed=8598903; DOI=10.1038/380041a0;
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
 RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
 RT "The crystal structure of the complex of blood coagulation factor VIIa
 RT with soluble tissue factor.";
 RL Nature 380:41-46(1996).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=99128538; PubMed=9925787; DOI=10.1006/jmbi.1998.2452;
 RA Zhang E., St Charles R., Tulinsky A.;
 RT "Structure of extracellular tissue factor complexed with factor VIIa
 RT inhibited with a BPTI mutant.";
 RL J. Mol. Biol. 285:2089-2104(1999).
 RN [10]
 RP STRUCTURE BY NMR OF 105-145.
 RX MEDLINE=98367502; PubMed=9692950; DOI=10.1021/bi980522f;
 RA Muranyi A., Finn B.E., Gippert G.P., Forsen S., Stenflo J.,
 RA Drakenberg T.;
 RT "Solution structure of the N-terminal EGF-like domain from human
 RT factor VII.";
 RL Biochemistry 37:10605-10615(1998).
 RN [11]
 RP VARIANT GLN-364.
 RX MEDLINE=91300046; PubMed=2070047;
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
 RA Meade T.W., Tuddenham E.G.D.;
 RT "Purification and characterization of factor VII 304-Gln: a variant
 RT molecule with reduced activity isolated from a clinically unaffected
 RT male.";
 RL Blood 78:132-140(1991).
 RN [12]
 RP VARIANTS GLN-364 AND PHE-370.
 RX MEDLINE=92340074; PubMed=1634227;
 RA Marchetti G., Patraccini P., Gemmati D., Derosa V., Pinotti M.,
 RA Rodorigo G., Casonato A., Girolami A., Bernardi F.;
 RT "Detection of two missense mutations and characterization of a repeat
 RT polymorphism in the factor VII gene (F7)." ;
 RL Hum. Genet. 89:497-502(1992).
 RN [13]
 RP VARIANT TYR-238.
 RX MEDLINE=93372811; PubMed=8364544;
 RA Marchetti G., Ferrati M., Patraccini P., Redaelli R., Bernardi F.;
 RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms
 RT (115His and 333Ser) in the human coagulation factor VII gene.";
 RL Hum. Mol. Genet. 2:1055-1056(1993).
 RN [14]
 RP VARIANTS.
 RX MEDLINE=94061028; PubMed=8242057;
 RA Takamiya O., Kembali-Cook G., Martin D.M.A., Cooper D.N.,
 RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,
 RA Tuddenham E.G.D., McVey J.H.;
 RT "Detection of missense mutations by single-strand conformational
 RT polymorphism (SSCP) analysis in five dysfunctional variants of

RT coagulation factor VII.";
 RL Hum. Mol. Genet. 2:1355-1359(1993).
 RN [15]
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.
 RX MEDLINE=94284305; PubMed=8204879;
 RA Chaing S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
 RT "Severe factor VII deficiency caused by mutations abolishing the
 RT cleavage site for activation and altering binding to tissue factor.";
 RL Blood 83:3524-3535(1994).
 RN [16]
 RP VARIANT SER-367.
 RX PubMed=7860081;
 RA Dewald G., Noehnen M.M., Ruther K.;
 RT "A common Ser/Thr polymorphism in the perforin-homologous region of
 RT human complement component C7.";
 RL Hum. Hered. 44:301-304(1994).
 RN [17]
 RP VARIANT VAL-354.
 RX MEDLINE=95072589; PubMed=7981691;
 RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
 RA Rodeghiero F., Marchetti G.;
 RT "Topologically equivalent mutations causing dysfunctional coagulation
 RT factors VII (294Ala-->Sval) and X (334Ser-->Pro)." ;
 RL Hum. Mol. Genet. 3:1175-1177(1994).
 RN [18]
 RP VARIANT MIE HIS-307.
 RX MEDLINE=95064662; PubMed=7974346;
 RA Ohiwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S., Suzuki K.;
 RT "Factor VII M1e: homozygous asymptomatic type I deficiency caused by
 RT an amino acid substitution of His (CAC) for Arg(247) (COC) in the
 RT catalytic domain.";
 RL Thromb. Haemost. 71:773-777(1994).
 RN [19]
 RP VARIANT MET-419.
 RX MEDLINE=96247510; PubMed=8652821;
 RA Arbini A.A., Mannucci P.M., Bauer K.A.;
 RT "A Thr359Met mutation in factor VII of a patient with a hereditary
 RT deficiency causes defective secretion of the molecule." ;
 RL Blood 87:5085-5094(1996).
 RN [20]
 RP VARIANTS TRP-283; LYS-325; VAL-358; GLN-364; GLU-402 AND GLN-413.
 RX MEDLINE=97001216; PubMed=8844208;
 RX DOI=10.1002/(SICI)1098-1004(1996)8:2<108::AID-HUMU23.3.CO;2-6;
 RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
 RA Lunghi B., Rodeghiero F., Marchetti G.;
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII
 RT deficiency." ;
 RL Hum. Mutat. 8:108-115(1996).
 RN [21]
 RP VARIANT VAL-304.
 RX MEDLINE=97037613; PubMed=8883260;
 RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M., Zaizov R.,
 RA Seligsohn U.;
 RT "Ala244Val is a common, probably ancient mutation causing factor VII
 RT deficiency in Moroccan and Iranian Jews." ;
 RL Thromb. Haemost. 76:283-291(1996).
 RN [22]
 RP VARIANT MORIOKA PRO-13.
 RX MEDLINE=98235713; PubMed=9576180;
 RA Ozawa T., Takikawa Y., Niiya K., Ejiri N., Suzuki K., Sato S.,
 RA Sakuragawa N.;
 RT "Factor VII Moriooka (FVII L-26P): a homozygous missense mutation in
 RT the signal sequence identified in a patient with factor VII
 RT deficiency." ;
 RL Br. J. Haematol. 101:47-49(1998).
 RN [23]
 RP VARIANTS MALTA THR-194 AND VAL-304.
 RX MEDLINE=98112461; PubMed=9452082;
 RA Alshinawi C., Scerri C., Gaidies R., Aquilina A., Felice A.E.;
 RT "Two new missense mutations (P134T and A244V) in the coagulation
 RT factor VII gene." ;

RL Hum. Mutat. Suppl. 1:S189-S191(1998).

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RN [24]
Query Match      81.2%; Score 161.5; DB 1; Length 466;
Best Local Similarity 75.6%; Pred. No. 8.5e-20;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 1 ANAYFLXXLRPGSLXRXKXCXQCFFXARXIFPKDAARTKLFWISY 45
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   61 ANA-FLEELRPGSLERECKEQCSFEAREIFKDAERTKLFWISY 104

RESULT 2
Q96PQ8 PRELIMINARY; PRT; 679 AA.
AC Q96PQ8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Factor VII active site mutant immunoconjugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;
RX Hu Z., Garen A.;
RA "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
RN [2]
SEQUENCE FROM N.A.
RP Hu Z., Garen A.;
RA Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RL ENBL; AF272774; AAKS8686.2; -.
DR HSSP; P08709; 1KLI.
DR GO; GO:0005576; C:cytoplasmic ion binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000152; ASx hydroxyl_S.
DR InterPro; IPR00742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR01254; Peptidase S1.
DR InterPro; IPR009003; Pept Ser.Cys.
DR InterPro; IPR000294; Vit_k_dep_GLA.
DR Pfam; PF07654; Cl-set; 2.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; Trypsin; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR KEGG-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 679 AA; 75552 MW; OB0023AE70A067A1 CRC64.
```


DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBLD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00998; GLA_2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Blood coagulation; Calcium-binding; Direct protein sequencing;
KW EGF-like domain; Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase;
KW Plasma; Repeat; Serine protease; Vitamin K; Zymogen.
FT CHAIN 1 152 Factor VII light chain.
FT CHAIN 153 407 Factor VII heavy chain.
FT DOMAIN 153 407
FT DOMAIN 1 45 Gla.
FT DOMAIN 46 82 EGF-like 1, calcium-binding (Potential).
FT DOMAIN 87 128 EGF-like 2.
FT DOMAIN 153 407 Serine protease.
FT SITE 152 153 Cleavage (by factor Xa, factor XIIa, factor IXa, or thrombin).
FT ACT_SITE 193 By similarity.
FT ACT_SITE 242 By similarity.
FT ACT_SITE 344 By similarity.
FT BINDING 338 Substrate (By similarity).
FT DISULFID 17 22 By similarity.
FT DISULFID 50 61 By similarity.
FT DISULFID 55 70 By similarity.
FT DISULFID 72 81 By similarity.
FT DISULFID 91 102 By similarity.
FT DISULFID 98 112 By similarity.
FT DISULFID 114 127 By similarity.
FT DISULFID 135 262 By similarity.
FT DISULFID 159 164 By similarity.
FT DISULFID 178 194 By similarity.
FT DISULFID 310 329 By similarity.
FT DISULFID 340 368 By similarity.
FT MOD_RES 6 6 4-carboxyglutamate.
FT MOD_RES 7 7 4-carboxyglutamate.
FT MOD_RES 14 14 4-carboxyglutamate.
FT MOD_RES 16 16 4-carboxyglutamate.
FT MOD_RES 19 19 4-carboxyglutamate.
FT MOD_RES 20 20 4-carboxyglutamate.
FT MOD_RES 25 25 4-carboxyglutamate.
FT MOD_RES 26 26 4-carboxyglutamate.
FT MOD_RES 29 29 4-carboxyglutamate.
FT MOD_RES 35 35 4-carboxyglutamate.
FT CARBOHYD 52 52 O-linked (GlcNAc...).
FT CARBOHYD 145 145 N-linked (GlcNAc...).
FT CARBOHYD 203 203 N-linked (GlcNAc...).
SQ SEQUENCE 407 AA; 44431 MW; 703E1FE06367F7E10 CRC64;

Query Match 56.8%; Score 113; DB 1; Length 407;
Best Local Similarity 51.2%; Pred. No. 3.1e-11;
Matches 21; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 5 FLXXLRPGSLRXCKXQCXCFXXARXIFKDXARTKLFWSY 45
DB 4 FLEELLPGSLRECRLECLSFEEAHEIFRNEERTQFWVSY 44

RESULT 6
Q8JHC9 PRELIMINARY; PRT; 443 AA.
AC Q8JHC9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Coagulation factor VIIi.
GN Names: f7i;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Hanumanthaiah R., Day K., Jagadeeswaran P.;
RT "Comprehensive analysis of blood coagulation pathways in Teleostei:
RT Evolution of coagulation factor genes and identification of zebrafish
RT factor VIIi.";
RL Blood Cells Mol. Dis. 0:0-0(2002).
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL; AF519546; AAM88342.1; -.
DR ENBL; AF515269; AAN71000.1; -.
DR HSPP; P00740; 1CFH.
DR ZFIN; ZDB-GENE-021206-10; f7i.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 443 AA; 48823 MW; 2D2504718A94FF4 CRC64;
Query Match 54.8%; Score 109; DB 2; Length 443;
Best Local Similarity 44.4%; Pred. No. 1.8e-10;
Matches 20; Conservative 8; Mismatches 17; Indels 0; Gaps 0;
QY 1 ANAYFLXLRPGSLRXCKXQCXCFXXARXIFKDXARTKLFWSY 45
DB 38 ANSGFLEEHKAGNLERECVEECIDYEAREVEFDDRTKQFWLSY 82
RESULT 7
PRTC_PIG STANDARD; PRT; 459 AA.
ID PRTC_PIG
AC Q9GLP2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Vitamin K-dependent protein C precursor (EC 3.4.21.69)
 DE (Autoproteolytic IIA) (Anticoagulant protein C) (Blood coagulation
 DE factor XIV)
 GN Name=PROG;
 OS Sub scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=21121490; PubMed=11229814;
 RA Gram D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,
 RA Kim H.K.W.;
 RT "Porcine factor V: cDNA cloning, gene mapping, three-dimensional
 RT protein modeling of membrane binding sites and comparative anatomy of
 RT domains.";
 RL Cell. Mol. Life Sci. 58:148-159 (2001).
 CC -!- FUNCTION: Protein C is a vitamin K-dependent serine protease that
 CC regulates blood coagulation by inactivating factors Va and VIIIa
 CC in the presence of calcium ions and phospholipids.
 CC -!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 CC and VIIIa.
 CC -!- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
 CC into a light chain and a heavy chain held together by a disulfide
 CC bond. The enzyme is then activated by thrombin, which cleaves a
 CC tetradecapeptide from the amino end of the heavy chain; this
 CC reaction, which occurs at the surface of endothelial cells, is
 CC strongly promoted by thrombomodulin.
 CC -!- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
 CC residues allows the modified protein to bind calcium.
 CC -!- MISCELLANEOUS: Calcium also binds, with stronger affinity to
 CC another site, beyond the GLA domain. This GLA-independent binding
 CC site is necessary for the recognition of the thrombin-
 CC thrombomodulin complex.
 CC -!- SIMILARITY: Belongs to the peptidase S1 family.
 CC -!- SIMILARITY: Contains 2 EGF-like domains.
 CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
 CC domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF191307; AAG28380.1; -.
 CC HSSP; P04070; 1AUT.
 CC MEROPS; S01_218; -.
 CC InterPro; IPR000152; Asx_hydroxyl_S.
 CC InterPro; IPR000742; EGF 2.
 CC InterPro; IPR001881; EGF Ca.
 CC InterPro; IPR006209; EGF like.
 CC InterPro; IPR002383; GLA blood.
 CC InterPro; IPR006210; IEGF.
 CC InterPro; IPR009003; Pept_Ser_Cys.
 CC InterPro; IPR001254; Peptidase_S1.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC InterPro; IPR000294; VitK_dep_GLA.
 CC Pfam; PF00008; EGF; 2.
 CC Pfam; PF00594; Gla; 1.
 CC Pfam; PF00089; Trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00001; GLABLOOD.
 CC SMART; SM00181; EGF; 2.
 CC SMART; SM00069; GLA; 1.
 CC SMART; SM00020; Tryp_SPc; 1.
 CC PROSITE; PS00010; ASX_HYDROXYL; 1.
 CC PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS00998; GLA_2; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Calcium-binding; EGF-like domain;
 KW Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;
 KW Repeat; Serine protease; Signal; Vitamin K.
 FT SIGNAL 1 18 By similarity.
 FT PROPEP 19 41 By similarity.
 FT CHAIN 42 459 Vitamin K-dependent protein C.
 FT CHAIN 42 196 Vitamin K-dependent protein C light chain
 FT CHAIN 199 459 (By similarity).
 FT CHAIN 199 459 (By similarity).
 FT PEPTIDE 199 213 Activation peptide (By similarity).
 FT SITE 213 214 Cleavage (by thrombin) (By similarity).
 FT DOMAIN 42 87 Gla.
 FT DOMAIN 96 131 EGF-like 1.
 FT DOMAIN 135 175 EGF-like 2.
 FT DOMAIN 214 459 Serine protease.
 FT MOD_RES 47 47 4-carboxyglutamate (By similarity).
 FT MOD_RES 48 48 4-carboxyglutamate (By similarity).
 FT MOD_RES 55 55 4-carboxyglutamate (By similarity).
 FT MOD_RES 57 57 4-carboxyglutamate (By similarity).
 FT MOD_RES 60 60 4-carboxyglutamate (By similarity).
 FT MOD_RES 61 61 4-carboxyglutamate (By similarity).
 FT MOD_RES 66 66 4-carboxyglutamate (By similarity).
 FT MOD_RES 67 67 4-carboxyglutamate (By similarity).
 FT MOD_RES 70 70 4-carboxyglutamate (By similarity).
 FT MOD_RES 112 112 3-hydroxyaspartate (By similarity).
 FT ACT_SITE 255 255 Charge relay system.
 FT ACT_SITE 301 301 Charge relay system.
 FT ACT_SITE 400 400 Charge relay system.
 FT DISULFID 58 63 By similarity.
 FT DISULFID 91 110 By similarity.
 FT DISULFID 100 105 By similarity.
 FT DISULFID 104 119 By similarity.
 FT DISULFID 121 130 By similarity.
 FT DISULFID 139 150 By similarity.
 FT DISULFID 146 159 By similarity.
 FT DISULFID 161 174 By similarity.
 FT DISULFID 182 321 Interchain (By similarity).
 FT DISULFID 240 256 By similarity.
 FT DISULFID 371 385 By similarity.
 FT DISULFID 396 424 By similarity.
 FT CARBOHYD 138 138 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 292 292 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 353 353 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;
 Query Match 52.0%; Score 103.5; DB 1; Length 459;
 Best Local Similarity 48.9%; Pred. No. 1.7e-09;
 Matches 22; Conservative 3; Mismatches 19; Indels 1; Gaps 1;
 Qy 1 ANAYFLXLRPGSLRXQXQCSFXRXARXFKDXRXTKLFWSY 45
 Db 42 ANS-FLBELPSSLERECKETCDFEAREIFQNTENTMAFWSKY 85
 RESULT 8
 PRTC MOUSE
 ID_PRTC_MOUSE STANDARD; PRTC; 460 AA.
 AC P33587; Q35498; Q91WN8; Q99PC6;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Vitamin K-dependent protein C precursor (EC 3.4.21.69)
 DE (Autoproteolytic IIA) (Anticoagulant protein C) (Blood coagulation
 DE factor XIV).


```

Biochem. J. 351:557-565(2000).
CC -1- SUBUNIT: Binds NEDD4 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- PM: Gla residues are produced after subsequent posttranslational
CC modifications of glutamate by a vitamin K-dependent gamma-
CC carboxylase (By similarity).
CC -1- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
CC domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: BC025098; AAH25098.1; -.
CC HSSP: P00740; 1CFH.
CC MIM: 604429; -.
CC GO: GO:0005515; F:protein binding; IPI.
CC InterPro: IPR002383; GLA_blood.
CC InterPro: IPR000294; VitK_dep_GLA.
CC Pfam: PF00594; Gla; 1.
CC PRINTS: PR00001; GLABLOOD.
CC SMART: SM00069; GLA; 1.
CC PROSITE: PS00011; GLA_1; 1.
CC PROSITE: PS00998; GLA_2; 1.
CC Gamma-carboxyglutamic acid; Signal; Transmembrane; Vitamin K.
KW SIGNAL 1 20
FT PROPEP 21 51
FT CHAIN 52 198
FT DOMAIN 52 111
FT TRANSMEM 112 134
FT DOMAIN 135 198
FT DOMAIN 52 97
FT SEQUENCE 198 AA; 23369 MW; 1C6482C8445450FC CRC64;
Query Match 48.2%; Score 96; DB 1; Length 198;
Best Local Similarity 44.4%; Pred. No. 1.6e-08;
Matches 20; Conservative 6; Mismatches 19; Indels 0; Gaps 0;
QY 1 ANAYFLXLRPGSLXRXCKXQCFFXARXIFKDXRTKLFWSY 45
Db 52 ANHWDLLELTPGNLERCLEERCSEAREYFDNTLTERFWESY 96
RESULT 11
TWG2 HUMAN STANDARD; PRT; 202 AA.
AC O14669;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Transmembrane gamma-carboxyglutamic acid protein 2 precursor (Proline-
DE rich Gla protein 2) (Proline-rich gamma-carboxyglutamic acid protein
DE 2).
DE Name=PRPG2; Synonyma=PRGP2, TWG2;
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97404347; PubMed=9256434; DOI=10.1073/pnas.94.17.9058;
RX Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
RT "Primary structure and tissue distribution of two novel proline-rich
RT gamma-carboxyglutamic acid proteins";
RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062 (1997).
CC -1- SUBUNIT: Binds NEDD4 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

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-1- TISSUE SPECIFICITY: Highly expressed in the thyroid.
CC -1- PM: Gla residues are produced after subsequent posttranslational
CC modifications of glutamate by a vitamin K-dependent gamma-
CC carboxylase.
CC -1- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
CC domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF009243; AB67071.1; -.
CC HSSP: P00740; 1CFH.
CC Genew; HGNC:9470; PRRG2.
CC MIM: 604429; -.
CC GO: GO:0005887; C:integral to plasma membrane; TAS.
CC InterPro: IPR002383; GLA_blood.
CC InterPro: IPR011047; Quin_alc_DH_like.
CC InterPro: IPR000294; VitK_dep_GLA.
CC Pfam: PF00594; Gla; 1.
CC PRINTS: PR00001; GLABLOOD.
CC SMART: SM00069; GLA; 1.
CC PROSITE: PS00011; GLA_1; 1.
CC PROSITE: PS00998; GLA_2; 1.
CC Gamma-carboxyglutamic acid; Signal; Transmembrane; Vitamin K.
KW SIGNAL 1 23
FT PROPEP 24 49
FT CHAIN 50 202
FT DOMAIN 50 109
FT TRANSMEM 110 132
FT DOMAIN 133 202
FT DOMAIN 50 96
FT DOMAIN 161 173
FT DOMAIN 191 194
FT SEQUENCE 202 AA; 22393 MW; BC79400C98492060 CRC64;
Query Match 48.2%; Score 96; DB 1; Length 202;
Best Local Similarity 44.4%; Pred. No. 1.6e-08;
Matches 20; Conservative 6; Mismatches 19; Indels 0; Gaps 0;
QY 1 ANAYFLXLRPGSLXRXCKXQCFFXARXIFKDXRTKLFWSY 45
Db 50 ANHWDLLELTPGNLERCLEERCSEAREYFDNTLTERFWESY 94
RESULT 12
Q6DIH4 PRELIMINARY; PRT; 216 AA.
AC Q6DIH4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Prig4-prov protein.
DE Name=prig4-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,

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RESULT 13
QB04XI1
ID Q804X1 PRELIMINARY; PRT; 442 AA.
AC Q804X1;
DT 01-JUN-2003 (trEMBLrel. 24, Created)
DT 01-JUN-2003 (trEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (trEMBLrel. 26, Last annotation update)
DE Coagulation factor VIIb (EC 3.4.21.21).
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxId=31033;
RN [1]
SEQUENCE FROM N.A.
RP Davidson C.J., Hirt R.P., Lal K., Snell P., Elgar G.,
RA Tuddenham E.G.D., McVey J.H.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL; AF465274; AAO33369.1; -.
DR HSSP; P00740; 1CFH.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0003802; F:coagulation factor VIIa activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.

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DR InterPro; IPR006210; IEGF
DR InterPro; IPR001234; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept Ser_Cys.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla_1.
DR Pfam; PF00089; Trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00069; GLA_1.
DR SMART; SM00020; Tryp_SPC_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 442 AA; 48787 MW; 810A561A127F0CF7 CRC64;

Query Match 47.2%; Score 94; DB 2; Length 442
Best Local Similarity 37.8%; Pred.No. 8.2e-08;
Matches 17; Conservative 11; Mismatches 17; Indels

Qy 1 ANAYFLXLRPGSLRXKXCXXQCSPFXARXIFKDAARTKLFWISY 45
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Db 38 ASGFGLEEMQQNLKECTIEICNYEAREVEFDDAQTKRFWEY 82

RESULT 14
R0804X7 PRELIMINARY; PRT; 425 AA.
AC Q804X7
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Coagulation factor VII (BC 3.4.21.21).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; P
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Davidson C.J., Hirt R.P., Lal K., Snell P., Elgar G.,
RA Tuddenham E.G.D., Mcvey J.H.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
CC -! SIMILARITY: Belongs to peptidase family S1.
CC -! SIMILARITY: Contains 1 EGF-like domain.
DR ENBL; AP465268; RAQ33363.1; -.
DR HSPG; P08709; IKDJ.
DR MSROPS; S01.215; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0003509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0003802; F:coagulation factor VIIa activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0004508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_I1.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept Ser_Cys.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_1.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2005, 09:42:23 ; Search time 30 Seconds
(without alignments)
111.974 Million cell updates/sec

Title: US10031005-3Y4

Perfect score: 199

Sequence: 1 ANAYFLXXLRPGSLRXCKX.....XXARXIFKDXRTKLFWISY 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.*
- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pap.*
 - 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap.*
 - 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pap.*
 - 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap.*
 - 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pap.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	161.5	81.2	44	3	US-08-955-636-3
2	161.5	81.2	44	4	US-09-302-239-3
3	161.5	81.2	44	4	US-09-497-591-3
4	161.5	81.2	44	4	US-09-803-810-3
5	161.5	81.2	406	1	US-08-293-778-24
6	161.5	81.2	406	1	US-08-295-411-5
7	161.5	81.2	406	2	US-08-953-471-5
8	161.5	81.2	406	4	US-09-782-587B-1
9	161.5	81.2	406	4	US-09-782-587B-3
10	161.5	81.2	406	5	PCT-US92-10242-5
11	161.5	81.2	444	1	US-08-475-845-2
12	161.5	81.2	444	2	US-08-327-690-2
13	161.5	81.2	444	2	US-08-660-289-2
14	161.5	81.2	444	2	US-08-537-807-2
15	161.5	81.2	444	2	US-08-871-003-2
16	161.5	81.2	444	3	US-08-464-233-2
17	161.5	81.2	444	3	US-09-189-607-2
18	161.5	81.2	444	3	US-09-378-907-2
19	161.5	81.2	444	5	PCT-US94-05779-2
20	161.5	81.2	461	4	US-09-949-016-8839
21	161.5	81.2	466	1	US-07-882-202A-4
22	161.5	81.2	466	1	US-08-021-615A-4
23	161.5	81.2	466	3	US-08-321-777-4
24	161.5	81.2	466	3	US-09-009-217-14
25	161.5	81.2	466	3	US-09-009-656-14
26	161.5	81.2	466	5	PCT-US93-04493-4
27	161.5	81.2	483	4	US-09-949-016-9523

28	155.5	78.1	44	3	US-08-955-636-29	Sequence 29, Appl
29	153.5	77.1	44	3	US-08-955-636-26	Sequence 26, Appl
30	153.5	77.1	44	3	US-08-955-636-27	Sequence 27, Appl
31	153.5	77.1	44	3	US-08-955-636-28	Sequence 28, Appl
32	149.5	75.1	44	3	US-08-955-636-30	Sequence 30, Appl
33	146.5	73.6	41	1	US-08-229-280-4	Sequence 4, Appl
34	142.5	71.6	42	4	US-09-383-667-7	Sequence 7, Appl
35	121	60.8	44	3	US-08-955-636-4	Sequence 4, Appl
36	121	60.8	44	4	US-09-302-239-4	Sequence 4, Appl
37	121	60.8	44	4	US-09-437-591-4	Sequence 4, Appl
38	121	60.8	44	4	US-09-803-810-4	Sequence 4, Appl
39	100.5	50.5	139	1	US-08-330-978-2	Sequence 2, Appl
40	100.5	50.5	139	1	US-08-474-042-2	Sequence 2, Appl
41	100.5	50.5	139	1	US-08-484-558-2	Sequence 2, Appl
42	100.5	50.5	139	1	US-08-774-592-2	Sequence 2, Appl
43	100.5	50.5	437	1	US-08-487-037-2	Sequence 2, Appl
44	100.5	50.5	437	1	US-08-487-037-3	Sequence 3, Appl
45	100.5	50.5	488	1	US-08-487-037-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-955-636-3
; Sequence 3, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-3

Query Match	81.2%	Score 161.5;	DB 3;	Length 44;
Best Local Similarity	97.8%	Pred. No. 1.1e-19;		
Matches	44;	Conservative	0;	Mismatches 1; Gaps 1;
Qy	1	ANAYFLXXLRPGSLRXCKXQCSFXXARXIFKDXRTKLFWISY	45	
Db	1	ANA-FLXXLRPGSLRXCKXQCSFXXARXIFKDXRTKLFWISY	44	

RESULT 2
US-09-302-239-3
; Sequence 3, Application US/09302239
; Patent No. 6693075
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary L.
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/09/302,239
; CURRENT FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-09-302-239-3

Query Match 81.2%; Score 161.5; DB 4; Length 44;
Best Local Similarity 97.8%; Pred. No. 1.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXLRPGSLXRCXKXQCXFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLXLRPGSLXRCXKXQCXFXXARXIFKDXRTKLFWISY 44

RESULT 3
US-09-497-591-3
Sequence 3, Application US/09497591
Patent No. 6747003
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary L.
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531-016001
CURRENT APPLICATION NUMBER: US/09/497,591
CURRENT FILING DATE: 2000-02-03
EARLIER APPLICATION NUMBER: 09/302,239
EARLIER FILING DATE: 1999-04-29
EARLIER APPLICATION NUMBER: 08/955,636
EARLIER FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-09-497-591-3

Query Match 81.2%; Score 161.5; DB 4; Length 44;
Best Local Similarity 97.8%; Pred. No. 1.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXLRPGSLXRCXKXQCXFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLXLRPGSLXRCXKXQCXFXXARXIFKDXRTKLFWISY 44

RESULT 4
US-09-803-810-3
Sequence 3, Application US/09803810
Patent No. 6762286
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary L.
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/09/803,810
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 44
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-09-803-810-3

Query Match 81.2%; Score 161.5; DB 4; Length 44;
Best Local Similarity 97.8%; Pred. No. 1.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXLRPGSLXRCXKXQCXFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLXLRPGSLXRCXKXQCXFXXARXIFKDXRTKLFWISY 44

RESULT 5
US-08-293-778-24
Sequence 24, Application US/08293778
Patent No. 5580560
GENERAL INFORMATION:
APPLICANT: Nicolaisen, Else M.
APPLICANT: Bjorn, Soren E.
APPLICANT: Wiberg, Finn C.
APPLICANT: Woodbury, Richard
TITLE OF INVENTION: MODIFIED FACTOR VII/VIII
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
FILING DATE:
APPLICATION NUMBER: DK 3235/87
FILING DATE: 25-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00103
FILING DATE: 24-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,248
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Agris, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129.224-US
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-293-778-24

Query Match 81.2%; Score 161.5; DB 1; Length 406;
Best Local Similarity 75.6%; Pred. No. 1e-18;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAYFLXLRPGSLXRCXKXQCXFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLYLRPGSLRYCKYQCXFFYARIFKDXRTKLFWISY 44


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RESULT 6
US-08-295-411-5
; Sequence 5, Application US/08295411
; Patent No. 5679639
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,411
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
;
; Query Match 81.2%; Score 161.5; DB 1; Length 406;
; Best Local Similarity 75.6%; Pred. No. 1e-18;
; Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 1 ANAYFLXLRPGSLRXCKXQCSEFXAXRIFKDAERTKLEWISY 45
DB 1 ANA-FLSELPGSLRECKEQCSFEAREIFKDAERTKLEWISY 44

RESULT 7
US-08-955-471-5
; Sequence 5, Application US/08955471
; Patent No. 5968751
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,411
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
;
; Query Match 81.2%; Score 161.5; DB 1; Length 406;
; Best Local Similarity 75.6%; Pred. No. 1e-18;
; Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 1 ANAYFLXLRPGSLRXCKXQCSEFXAXRIFKDAERTKLEWISY 45
DB 1 ANA-FLSELPGSLRECKEQCSFEAREIFKDAERTKLEWISY 44

RESULT 8
US-09-782-587B-1
; Sequence 1, Application US/09782587B
; Patent No. 6806063
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUD
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26
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; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,471
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/295,411
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
;
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
;
; US-08-955-471-5
;
; Query Match 81.2%; Score 161.5; DB 2; Length 406;
; Best Local Similarity 75.6%; Pred. No. 1e-18;
; Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 1 ANAYFLXLRPGSLRXCKXQCSEFXAXRIFKDAERTKLEWISY 45
DB 1 ANA-FLSELPGSLRECKEQCSFEAREIFKDAERTKLEWISY 44

RESULT 8
US-09-782-587B-1
; Sequence 1, Application US/09782587B
; Patent No. 6806063
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUD
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26
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Query Match 81.2%; Score 161.5; DB 4; Length 406;
Best Local Similarity 75.6%; Pred. No. 1e-18;

US-08-475-845-2

RESULT 11
US-08-475-845-2

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1 NUMBER OF SEQUENCES: 4
2 CORRESPONDENCE ADDRESS:
3 ADDRESSEE: Townsend and Townsend Kourie and Crew
4 STREET: One Market Plaza, Steuart Street Tower
5 CITY: San Francisco
6 STATE: CA
7 COUNTRY: U.S.A.
8 ZIP: 94105-1492
9 COMPUTER READABLE FORM:
10 MEDIUM TYPE: Floppy disk
11 OPERATING SYSTEM: IBM PC compatible
12 SOFTWARE: PatentIn Release #1.24
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/327,690
15 FILING DATE: 24-OCT-1994
16 CLASSIFICATION: 435
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: 08/065,725
19 FILING DATE: 21-MAY-1993
20 CLASSIFICATION: 435
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: 07/662,920
23 FILING DATE: 28-FEB-1991
24 CLASSIFICATION: 435
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Parmelee, Steven W.
27 REGISTRATION NUMBER: 31,990
28 REFERENCE/DOCKET NUMBER: 13952-8-3
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: 206-467-9600
31 TELEFAX: 415-543-5043
32 INFORMATION FOR SEQ ID NO: 2:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 444 amino acids
35 TYPE: amino acid
36 TOPOLOGY: linear
37 MOLECULE TYPE: protein
38 US-08-327-690-2
39
40 Query Match 81.2%; Score 161.5; DB 2; Length 4
41 Best Local Similarity 75.6%; Pred.No.1.1e-18;
42 Matches 34; Conservative 0; Mismatches 10; Indels
43
44 QY 1 ANAYFLXLRPGSLRXRCXQCSPXXARXIFPDAXRTKLFWISY 45
45 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
46 DB 39 ANA-FLBRLPGSLRCKEKEQCSFEAREIFKDAERTKLFWISY 82
47
48 RESULT 13
49 US-08-660-289-2
50 Sequence 2, Application US/08660289
51 Patent No. 5833982
52 GENERAL INFORMATION:
53 APPLICANT: Berkner, Kathleen L.
54 APPLICANT: Petersen, Lars C.
55 APPLICANT: Hart, Charles E.
56 APPLICANT: Hedner, Ulla
57 APPLICANT: Bregengaard, Claus
58 TITLE OF INVENTION: Modified Factor VII
59 NUMBER OF SEQUENCES: 4
60 CORRESPONDENCE ADDRESS:
61 ADDRESSEE: Townsend and Townsend Kourie and Crew
62 STREET: One Market Plaza, Steuart Street Tower
63 CITY: San Francisco
64 STATE: CA
65 COUNTRY: U.S.A.
66 ZIP: 94105-1492
67 COMPUTER READABLE FORM:
68 MEDIUM TYPE: Floppy disk
69 OPERATING SYSTEM: IBM PC compatible
70 SOFTWARE: PatentIn Release #1.24

```


RESULT 2
US-10-298-330-3


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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-587B-3

Query Match      81.2%; Score 161.5; DB 10; Length 406;
Best Local Similarity 75.6%; Pred. No. 4.1e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAYFLXLRPGSLRXCKXXQCSPFXRXARXIFKDXRXTKLFWISY 45
Db 1 ANA-FLEELRPGSLRECKEQCSPFEAREIFKDXRXTKLFWISY 44

RESULT 6
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286.200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; CURRENT FILING DATE: 2002-03-22
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match      81.2%; Score 161.5; DB 14; Length 406;
Best Local Similarity 97.8%; Pred. No. 4.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXLRPGSLRXCKXXQCSPFXRXARXIFKDXRXTKLFWISY 45
Db 1 ANA-FLLXLRPGSLRXCKXXQCSPFXRXARXIFKDXRXTKLFWISY 44

RESULT 7
US-10-255-032-1
; Sequence 1, Application US/10255032
; Publication No. US20030100075A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030100075A10 No. US20030100075Aldisk A/S
; TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
; FILE REFERENCE: 6357-WO
; CURRENT APPLICATION NUMBER: US/10/255,032
; CURRENT FILING DATE: 2002-09-24
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: DK PA 2001 01413
; PRIOR FILING DATE: 2001-09-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: human coagulation Factor VII
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate)
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US-10-255-032-1

Query Match      81.2%; Score 161.5; DB 14; Length 406;
Best Local Similarity 97.8%; Pred. No. 4.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXLRPGSLRXCKXXQCSPFXRXARXIFKDXRXTKLFWISY 45
Db 1 ANA-FLLXLRPGSLRXCKXXQCSPFXRXARXIFKDXRXTKLFWISY 44

RESULT 8
US-10-281-727-1
; Sequence 1, Application US/10281727
; Publication No. US20030130191A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Human Coagulation Factor VII
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 6410.200-US
; CURRENT APPLICATION NUMBER: US/10/281,727
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PA 2001 01627
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 60/335,383
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid
; OTHER INFORMATION: (gamma-carboxyglutamate)
US-10-281-727-1

Query Match      81.2%; Score 161.5; DB 14; Length 406;
Best Local Similarity 97.8%; Pred. No. 4.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXLRPGSLRXCKXXQCSPFXRXARXIFKDXRXTKLFWISY 45
Db 1 ANA-FLLXLRPGSLRXCKXXQCSPFXRXARXIFKDXRXTKLFWISY 44

RESULT 9
US-10-386-898-7
; Sequence 7, Application US/10386898
; Publication No. US20030229018A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030229018A10 No. US20030229018Aldisk Pharmaceuticals, Inc.
; APPLICANT: Kjalke, Marianne
; APPLICANT: Jakobsen, Palle
; APPLICANT: Stennicke, Henning Ralf
; TITLE OF INVENTION: DIMERIC TF ANTAGONIST
; FILE REFERENCE: 6445.200-US
; CURRENT APPLICATION NUMBER: US/10/386,898
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: Danish Application PA 2002 00373
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US 60/365,935
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 406
; TYPE: PRT
; ORGANISM: human coagulation Factor VII
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)...(406)
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OTHER INFORMATION: Xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate)
US-10-386-898-7

Query Match 81.2%; Score 161.5; DB 15; Length 406;
Best Local Similarity 97.8%; Pred. No. 4.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLXRXCKXXQCSFXXARXIFKDXRXTKLFWISY 45
Db 1 ANA-FLXXLRPGSLXRXCKXXQCSFXXARXIFKDXRXTKLFWISY 44

RESULT 10

US-10-383-898-1
; Sequence 1, Application US/10383898
; Publication No. US20040009914A1
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: Curcuminoid-protein conjugates
; FILE REFERENCE: E056 1060.1
; CURRENT APPLICATION NUMBER: US/10/383,898
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (1)..(406)

US-10-383-898-1

Query Match 81.2%; Score 161.5; DB 15; Length 406;
Best Local Similarity 75.6%; Pred. No. 4.1e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLXRXCKXXQCSFXXARXIFKDXRXTKLFWISY 45
Db 1 ANA-FLEELRPGSLERECKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 11

US-10-617-500-1
; Sequence 1, Application US/10617500
; Publication No. US20040072753A1
; GENERAL INFORMATION:
; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
; APPLICANT: Stennicke, Henning R
; APPLICANT: Bjorn, Soren E
; APPLICANT: Petersen, Lars C
; TITLE OF INVENTION: TF Antagonist
; FILE REFERENCE: 6510.200-US
; CURRENT APPLICATION NUMBER: US/10/617,500
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01100
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/404,567
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(406)
; OTHER INFORMATION: Xaa=4-carboxyglutamic acid (gamma-carboxyglutamate)
US-10-617-500-1

Query Match 81.2%; Score 161.5; DB 15; Length 406;
Best Local Similarity 97.8%; Pred. No. 4.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLXRXCKXXQCSFXXARXIFKDXRXTKLFWISY 45
Db 1 ANA-FLXXLRPGSLXRXCKXXQCSFXXARXIFKDXRXTKLFWISY 44

RESULT 12

US-10-263-205B-2
; Sequence 2, Application US/10263205B
; Publication No. US20040087498A1
; GENERAL INFORMATION:
; APPLICANT: BERKNER, Kathleen L.
; APPLICANT: PETERSEN, Lars
; APPLICANT: HART, Charles E.
; APPLICANT: HEDNER, Ulla
; APPLICANT: BREGENGAARD, Claus
; TITLE OF INVENTION: MODIFIED FACTOR VII
; FILE REFERENCE: 13952N-8-5-1
; CURRENT APPLICATION NUMBER: US/10/263,205B
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 08/464,029
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/327,690
; PRIOR FILING DATE: 1994-10-24
; PRIOR APPLICATION NUMBER: PCT/US94/05779
; PRIOR FILING DATE: 1994-05-23
; PRIOR APPLICATION NUMBER: 08/065,725
; PRIOR FILING DATE: 1993-05-21
; PRIOR APPLICATION NUMBER: PCT/US92/01636
; PRIOR FILING DATE: 1991-02-28
; PRIOR APPLICATION NUMBER: 07/662,920
; PRIOR FILING DATE: 1991-02-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-263-205B-2

Query Match 81.2%; Score 161.5; DB 15; Length 406;
Best Local Similarity 75.6%; Pred. No. 4.1e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLXRXCKXXQCSFXXARXIFKDXRXTKLFWISY 45
Db 1 ANA-FLEELRPGSLERECKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 13

US-10-617-619-1
; Sequence 1, Application US/10617619
; Publication No. US20040110929A1
; GENERAL INFORMATION:
; APPLICANT: Bjorn, Soren E
; APPLICANT: Nicolaisen, Else M
; APPLICANT: Jorgensen, Anker S
; TITLE OF INVENTION: TF Binding Compound
; FILE REFERENCE: 6455.200-US
; CURRENT APPLICATION NUMBER: US/10/617,619
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01099
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/404,568
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT


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; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(406)
; OTHER INFORMATION: Xaa=4-carboxyglutamic acid (gamma-carboxyglutamate)
US-10-617-619-1

Query Match      81.2%; Score 161.5; DB 16; Length 406;
Best Local Similarity 97.8%; Pred. No. 4.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLRXKCKXXQCSPXXARXIFKDXARTKLFWISY 45
Db 1 ANA-FLXXLRPGSLRXKCKXXQCSPXXARXIFKDXARTKLFWISY 44

RESULT 14
US-10-701-294-1
; Sequence 1, Application US/10701294
; Publication No. US20040143099A1
; GENERAL INFORMATION:
; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
; APPLICANT: Petersen, Lars C
; APPLICANT: Back, Jakob M
; APPLICANT: Meyer, Christian
; TITLE OF INVENTION: Pharmaceutical Composition Comprising a Tissue Factor Antagonist
; TITLE OF INVENTION: and a Blood Glucose Regulator
; FILE REFERENCE: 6608.200-US
; CURRENT APPLICATION NUMBER: US/10/701,294
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: US 60/434,904
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01710
; PRIOR FILING DATE: 2002-11-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: human coagulation Factor VII
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(406)
; OTHER INFORMATION: Xaa=4-carboxyglutamic acid (gamma-carboxyglutamate)
US-10-701-294-1

Query Match      81.2%; Score 161.5; DB 16; Length 406;
Best Local Similarity 97.8%; Pred. No. 4.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLRXKCKXXQCSPXXARXIFKDXARTKLFWISY 45
Db 1 ANA-FLXXLRPGSLRXKCKXXQCSPXXARXIFKDXARTKLFWISY 44

RESULT 15
US-10-669-537-1
; Sequence 1, Application US/10669537
; Publication No. US20040192602A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; APPLICANT: Olsen, Ole Hvilsted
; TITLE OF INVENTION: Human Coagulation Factor VII Polypeptides
; FILE REFERENCE: 6544.200-US
; CURRENT APPLICATION NUMBER: US/10/669,537
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01423
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 60/417,927
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 13
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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(406)
; OTHER INFORMATION: Xaa=carboxyglutamic acid (gamma-carboxyglutamate)
US-10-669-537-1

Query Match      81.2%; Score 161.5; DB 16; Length 406;
Best Local Similarity 97.8%; Pred. No. 4.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLRXKCKXXQCSPXXARXIFKDXARTKLFWISY 45
Db 1 ANA-FLXXLRPGSLRXKCKXXQCSPXXARXIFKDXARTKLFWISY 44

Search completed: August 22, 2005, 19:20:43
Job time : 663 secs
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